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A;Title: Fatty acylation of two internal lysine residues required for the toxic activity A;Reference number: A55387; MUID:95099325; PMID:7801126
A;Reference number: Jysine palmitoylation
A;Contents: annotation; lysine palmitoylation
A;Note: lysine modification is performed by the hlyC gene product
B;Haertlein, M.; Schiess1, S.; Wagner, W.; Rdest, U.; Kreft, J.; Goebel, W.
A;Title: Transport of hemolysin by Escherichia coli.
A;Reference number: 141280
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C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
E;246-791/Domain: hemolysin A homology - 4HIVA>
E;246-791/Domain: hemolysin A homology - 4HIVA>
E;723-681/Region: 9-residue repeats (G-X-G-[IN]-D-X-[INIYF]-X)
E;563,689/Binding site: palmitate (Lys) (covalent) #status experimental
R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner, F.R.
Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence plasmid of Escher
A;Reference number: Z22068; MUID:98391744; PMID:9722640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1023 <FEL>
A;Residues: 1-1023 <FEL>
A;Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; PID:g146379
A;Experimental source: strain J96, O4 serotype
A;Experimental source: b.C.; Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
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Cippedies: Becherichia coli
Cipate: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 18-Jun-1999
CiAccession: A24433; 141288
Airlie: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.
Airlie: Nucleotide sequence of an Escherichia coli chromosomal hemolysin.
Aireference number: A24433; MUID:85234404; PMID:3891743
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A;Molecule type: DNA
A;Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A;Cross_references: GB:M29173; NID:g146337; PIDN:AAA23957.1; PID:g146338
                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; hipoprotein; toxin
F;233-776/Domain: hemolysin A homology <HLYA>
F;SSO,675/Binding site: palmitate (Lys) (covalent) #status predicted
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Pred. No. 6.4e-05;
0; Mismatches 0; Indels
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Pred. No. 6.2e-05;
                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF074613; PIDN:AAC70116.1
A;Experimental source: strain EDL933; serotype 0157:H7
                                                                                                          A; Accession: T42148
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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Best Local Similarity
Matches 14; Conserv
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C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: 13.449-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: 141078
R;Schmidt, H.; Beutin, L.; Karch, H.
Infect: Immun. 63, 1055-1061, 1995
A;Title: Molecular analysis of the plasmid-encoded hemolysin of Escherichia coli 0157:H7
A;Reference number: 141077; MUID:95172699; PMID:7868227
A;Reference number: 141077
A;Accession: 141078
A;Residues: I-998 cRES>
A;Residues: 1-998 cRES>
A;Coression: Infect: MRBL:X79839; NID:9860324, PIDN:CAA56234.1; PID:94388764
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: lipoprotein
F;233-776/Domain: hemolysin A homology curvalent) #status predicted
F;550,675/Binding site: palmitate (Lys) (covalent)
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T18074
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S61904
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A;Title: Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin Il A;Reference number: A49219; WUID:93162836; PMID:8432615 A;Accession: B49219
                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain 405, serotype 8
A;Note: sequence extracted from NCB1 backbone (NCBIN:125168, NCBID:125170)
R;Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
Infect. Immun. 62, 4411-4418, 1994
A;Title: Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: chan A;Reference number: $48042; MUID:95012630; PMID:7927703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Description: lyses lung macrophages
C, Superfamily: hemolysin A; hemolysin A homology
C, Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat; thiolester
F;254-804/Domain: hemolysin A homology <HLXA>
F;736-862/Region: 9-residue repeate (G-C.X-G-[DN]-D-X-[LVIYF]-X)
F;71,702/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain 405, serotype 8
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Comment: This orgnism causes porcine pleuropneumonia.
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R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, A.L.J.
Infect. Immun. 59, 4497-4504, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; nucleic acid sequence not shown; translation not shown
              ;Species: Actinobacillus pleuropneumoniae;
;Date: 19-Dec-1993 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
;Accession: B49219; S48043; S29958
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C;Species: Actinobacillus pleuropneumoniae
C;Date: 09-Mar-1990 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B31389; S18853; B43599
R;Chang, Y.F.; Young, R.; Struck, D.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Residues: 1-1052 <JAN2>
;Cross-references: EMBL:X80055; NID:g558150; PIDN:CAA56358.1; PID:g558152
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                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1052 <JAN1>
A;Cross-references: EMBL:X68815; NID:g38956; PIDN:CAA48711.1; PID:g38958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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6.5e-05;
hes 0; Indels
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R;Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp,
submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cytolysins of Actinobacillus pleuropneumoniae 1
A;Reference number: A43599; MUID:92040145; PMID:1937809
                                                                                                                              Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.;
nfect. Immun. 61, 947-954, 1993
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1.5%; Score 14; DB
Best Local Similarity 100.0%; Pred. No. 6.5
Matches 14; Conservative 0; Mismatches
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A,Molecule type: DNA
A,Residues: 1-956 <CHA>
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                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
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Coxin III - Actinobacillus pleuropneumoniae (serotype 2)

NyAlternate names: RTX-toxin IIIA (ApxIIIA)

C;Species: Actinobacillus pleuropneumoniae

C;Date: 14-Jul-1995 #sequence_revision 15-Nov-1996 #text_change 18-Jun-1999

C;Accession: S51784

R;Chang, Y.F.; Shi, J.; Ma, D.P.; Shin, S.J.; Lein, D.H.

DNA Cell Biol. 12, 351-362, 1993

A;Title: Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cl
                                                                                                                                                                                                  C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
C;Accession: S10056
R;Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
R;Hess, J.; Wels, W.; Vogel, M.; Goebel, W.
R;Hess Microbiol. Lett. 34, 1-11, 1986
A;Title: Nucleoride sequence of a plasmid-encoded hemolysin determinant and its comparis
A;Reference number: S07209
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F;735-861/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;571,702/Binding site: palmitate (Lys) (covalent) #status predicted
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A;Molccule type: DDA
A;Residues: 1-1049 <CHA>
A;Residues: 1-1049 <CHA>
A;Cross-references: EMBL:L12145; NID:g349605; PIDN:AAA21924.1; PID:g470685
C;Comment: This orgnism causes porcine pleuropneumonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: hemolygin A; hemolysin A homology
C;Kaywords: lipoprotein
F:247-72/Domain: hemolysin A homology <HLVA>
F:564,690/Binding site: palmitate (Lys) (covalent) #status predicted
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100.0%; Pred. No. 6.5e-05;
tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 14; Conservative 0; Mismatches 0;
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                                                                                                                                                                     hemolysin A - Escherichia coli plasmid pHly152
405 ISGILEASKQAMFE 418
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A;Cross-references: EMBL:M14107
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Best Local Similarity 100.
Matches 14; Conservative
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A;Cross-references: EMBL:X73117; NID:g312897; PIDN:CAA51548.1; PID:g312899
R;Frey, J.; Meier, R.; Gygi, D.; Nicolet, J.
Infect: Immun. 59, 3026-5932, 1991
A;Title: Nuclectide sequence of the hemolysin I gene from Actinobacillus pleuropneumoniae A;Reference number: S18769; MUID:91348845; PMID:187928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Sequence analysis and transcription of the apxI operon (hemolysin I) from Actino (Reference number: I39644; MUID:94237497; PMID:8181764 ,Accession: I39645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Modecule type: DNA
A; Residues: 1-209, 'AMPXLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Residues: 1-209, 'AMPXLTLA', 218-373, 'R', 375-561, 'Q', 563-686, 'TC', 688-1022 <RE2>
A; Cross-references: EMBL: X68555; NID: 9505568; PIDN: CAA48586.1; PID: 9505570
R; Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.; Rodn
Mol. Microbiol. 14; 207-216, 1994
A; Title: The RTX haemolysins ApxI and ApxII are major virulence factors of the swine path
A; Reference number: 860731; MUID: 95131743; PMID: 7830567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBI
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C; Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
E; 243.799 Domain: hemolysin A homology <HLYA>
F; 243.799 Domain: hemolysin A homology <HLYA>
F; 721.847/Region: 9-residue repeats (G-X-G-[IN]-D-X-[INIYF]-X)
F; 560,686/Binding site: palmitate (Lys) (covalent) #status predicted
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y, Molecule type: DNA
y, Residues: 1-953 <HIG>
y, Strathdee, C.A., Lo, R.Y.C.
y, Strathdee, C.A., Lo, R.Y.C.
y, Title: Cloning, nucleotide sequence, and characterization of genes encoding the y, Reference number: A32051; MUID:89123172; PMID:2914876
                                                                                                                                                                                                                                                                                                                        A;Residues: 1-209,'AMPYLTLA',218-373,'R',375-561,'Q',563-686,'TC',688-1022 <FRE>A;Cross-references: EMBL:X52899; NID:g38949; PIDN:CAA37081.1; PID:g38950
R;Frey, J.; Haldimann, A.; Nicolet, J.; Boffini, A.; Prentki, P.
Gene 142, 97-102, 1994
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C;Species: Pasteurella haemolytica
C;Date: 12-Oct-1989 Haequence zevision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: B30169; C32051; S2916
B;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
A;Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A;Reference number: A30169; MUID:89210283; PMID:2707120
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C;Comment: This organism causes porcine pleuropneumonia.
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100.0%; Pred. No. 0.066;
1ve 0; Mismatches 0;
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R;LO, R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
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Matches 11; Conserv
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C, Function:
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N;Alternate names: ashA protein; cytolysin II; RTX-toxin II
C;Species: Actinobacillus suis
C;Species: Actinobacillus suis
C;Date: 31-Dec-1993 #sequence_revision 08-Nov-1996 #text_change 05-Dec-1998
C;Accession: A43834
C;Accession: A43834
Infect. Immun. 60, 2166-2173, 1992
A;Title: Molecular characterization of an RTX toxin determinant from Actinobacillus suis
A;Reference number: A43834; MUID:92267623; PMID:1587585
A;Accession: A43834
A;Molecule type: DNA
A;Reference number: BNA
A;Resprimental Bource: isolate 3714
A;Note: sequence extracted from NCBI backbone (NCBIN:104212, NCBIP:104211)
C;Comment: This organism causes acute fatal septicemia in young pigs.
C;Comment: This organism causes acute fatal septicemia in young pigs.
C;Comment: attacks cell membranes and causes cell lysis
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; lipoprotein; tandem repeat;
F;24-787/Domain: hemolysin A homology *RiXA>
F;719-801/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;557/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTX-toxin I - Actinobacillus pleuropneumoniae

NyAlternate names: hemolysin ApxI

NyAlternate names: hemolysin ApxI

NyAlternate names: hemolysin ApxI

NyAlternate names: hemolysin ApxI

Cybecies: Actinobacillus pleuropneumoniae

Cybecies: 19-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999

Cybecession: 13664; S60732; S36781

Cybecession: 13664; S60732; S36781

A.Title: Briaire, J.; Kamp. E.M.; Gielkens, A.L.; Smits, M.A.

Infect. Immun. 61, 3688-3695, 1993

A.Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI) c

A;Reference number: 139641; MUID:93366425; PMID:8359891

A;Recession: 139643

A;Accession: 139643

A;Molecule type: DNA
A;Accession: B43599
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolacule type: DNA
A;Crowsert: This organism causes porcine pleuropneumonia.
C;Genetics:
A;Gene: apxIIA; appA; clyIIA
C;Function:
A;Description: attacks blood cell membranes and causes cell lysis
C;Superfamily: hemolysin A, hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F;243-787/Bomain: hemolysin A, homology
F;719-801/Region: 9-residue repeats (G-G-X-C-[DNI-D-X-[LNIYF]-X)
F;557/Binding site: palmitate (Lys) (covalent) #status predicted
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00.0%; Pred. No. 0.062;
ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 ALLVAGVTGLI 379
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secret

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mannuronan C-5-epimerase (EC 5.1.3.-) - Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Accession: 877624
R;Ertesvaag, H.; Hoeidal, H.K.; Hals, I.K.; Rian, A.; Doseth, B.; Valla, S.
A)Cl. Microbiol. 16, 719-711, 1995
A;Title: A family of modular type mannuronan C-5-epimerase genes controls alginate struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Description: catalyzes the Ca(2+)-dependent epimerization of D-mannuronic acid residues
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; WUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000020; PIDN:BAB78388.1; PID:g17135842; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1403 <ERT>
A;Cross-references: EMBL:L39096; NID:g790690; PIDN:AAA87311.1; PID:g790692
A;Experimental source: strain E
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      F;745-753/Region: repeat
F;754-762/Region: repeat
F;763-771/Region: repeat
F;772-780/Region: repeat
F;792-80/Region: repeat
F;92-80/Region: repeat
F;801-809/Region: repeat
F;801-809/Region: repeat
F;556/Binding site: palmitate (Lys) (covalent) #status predicted
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0.62;
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0.88;
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100.0%; Pred. No.
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100.0%; Pred. No.
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A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Pathway: alginate biosynthesis
C,Keywords: calcium binding; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 10; Conservative
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285 LAQRVAAGLS
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A;Genome: plasmid
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C;Function:
                                                                                                                                                                                                                                                                                            Query Match
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A;Molecule type: DNA
A;Crose-references: GB:M24197; GB:M34943; GB:M34944
B;Lainson, A.F.; Aitchison, K.D.; Donachie, W.
Bubmitted to the EMBL Data Library, June 1993
A;Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 serc
A;Reference number: S34235
A;Accession: S34237
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C;Superfamily: hemolysin A; hemolysin A homology
C;Superfamily: hemolysin B; hemolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
F;240-786/Domain: hemolysin A homology «HLYA»
F;18-805/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;718-726/Region: repeat
F;718-726/Region: repeat
                                                                                                                                                                                                                                                                                  C.Function:
A.Description: lyees leukocytes
A.Description: lyees leukocytes
A.Description: lyees leukocytes
C.Superfamily: hemolysin A. homology
C.Steywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
E.238-784/Domain: hemolysin A. homology <HLXA>
E.218-784/Domain: hemolysin A. homology <HLXA>
E.716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
E.554/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukotoxin A - Pasteurella haemolytica (serotype T10)
N.Alternate names: lktA protein
C;Species: Pasteurella haemolytica
C;Species: 10-Aug-1990 Haequence revision 15-Nov-1996 #text_change 18-Jun-1999
C;Accession: 33745; A35254; S34337; S34235
R;Lainson, A.F.; Aitchison, K.; Donachie, W.
submitted to the BMBL Data Library, September 1993
A;Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype. A;Reference number: S37145
A;Title: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al.
A;Reference number: S29515; MUID:87306837; PMID:3040588
A;Accession: S29516
                                                                                                     A;Molecule type: DNA
A;Residues: 1-741,'D',743-953 <LOR>
A;Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
C;Genetics:
A;Gene: lktA
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A; Residues: 1-955 <LAI>
A; Residues: 1-955 <LAI>
A; Cross-references: EMBL: 226247; NID: 9400424; PIDN: CAA81206.1; PID: 9400425
R; Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A; Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A; Reference number: A35254; MUID: 90236888; PMID: 2185213
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A;Residues: 745-955 <LA2>
A;Residues: 745-955 <LA2>
A;Experimental source: EMBL:222884; NID:g311828; PIDN:CAA80498.1; PID:g311829
A;Experimental source: serotype T3
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Modicoule type: DNA
A,Residues: 723-955 <LA3>
A,Cross-references: EMBL:Z22887; NID:g311824; PIDN:CAA80501.1; PID:g311825
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100.0%; Pred. No. 0.62;
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Matches 10; Conservative
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C;Species: Pasteurella haemolytica
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C;Accession: S34239, S34239, S34239, S34239, S34239, Satchison, A.F.; Aitchison, K.D.; Donachie, W. submitted to the EMBL Data Library, June 1993
A;Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T4 sero of Pasturella haemolytica.
A;Reference number: S34236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: AD0468
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein YPO3844 [imported] - Yersinia pestis (strain CO92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Accession: S34236
A,Molecule type: DNA
A,Residues: 9-208 - 1.42>
A,Cross-references: EMBL:Z22886; NID:g311826; PIDN:CAA80500.1; PID:g311827
A,Experimental source: serotype T15
                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-208 <LAI>
A;Cross-references: EMBL:Z22885; NID:g311830; PIDN:CAA80499.1; PID:g311831
A;Experimental source: serotype T4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             725 DRLFGGKG 732
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A;Molecule type: DNA
A;Residues: 1-234 <KUR>
                                                                                                                                                                                                                                                                                                        A; Accession: S34238
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A;Gene: YPO3844
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                                                                                                                                                                                                                                                                                                                      ATP synthase B chain atpF [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C; Species: Agrobacterium tumefaciens C; Species: A; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Atthers: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W. A; Reference number: AB2577; MUID:21608550; PMID:11743193 Agrobacterium tumefaciens C58. A; Accession: Ad2664 A; Status: preliminary A; MUID:21608550; PMID:11743193 A; Residues: 1-161 «KUR» A; Residues: GB:AE008688; PIDN:AAL41733.1; PID:g17739083; GSPDB:GN00186 A; Experimental source: strain C58 (Dupont) C; Genetics: A; Genetics: A; Genetics: A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AGR C 1301 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium_tumefaciens C; Space: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C; Adcession: F97446 A; Liu, F; Wollam, C.; Allinger, M.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, Science 294, 2322-2328, 2001 A; Miller, M.; Boughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A; Eference number: A97359; MUD:21608551; PMID:11743194 A; Reference number: A97359; MUD:21608551; PMID:11743194 A; Residum tumefaciens: A; Residues: P97446 A; Residues: P97446 A; Residues: P97446 A; Residues: DNA A; Residues: DNA A; Residues: 1-161 - KUR> A; Cross-references: GB:AE007869; PIDN:AAK86527.1; PID:g15155685; GSPDB:GN00169
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   Pred. No. 2.7;
Mismatches
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leukotoxin A - Pasteurella haemolytica (fragment)
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      100.0%;
Similarity 100.
10; Conservative
                                                                                                                                                                4296 DVLNGGAGND 4305
                                                                                                 752 DVLNGGAGND 761
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   Best Local
Matches 1
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Length 270 0; Indels

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A;Accession: JE0183
A;Molecule type: protein
A;Residues: 1-275 <YAM-
C;Comment: This enzyme catalyzes the hydrolysis of beta-1,4-linked homopolymers or oligor
C;Superfamily: alcohol sulfotransferase
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Comment: This enzyme, a member of class III plant chitinases, which catalyzes the hydro
or protection against fungal pathogens.
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Ateres: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AD3003
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
                                                                                                                                                                                                                                                                                                                                  JE0183

Achitimase (EC 3.2.1.14) 1 - cone shell (Conus tulipa)

NyAlternate names: TBC-1

C;Species: Conus tulipa (tulip cone)

C;Species: L-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 07-May-1999

C;Accession: JE0183

R;Yamagami, T.; Ishiguro, M.

Bisscl: Biotechnol. Biochem. 62, 1253-1257, 1998

A;Title: Complete anino acid sequences of chitimase-1 and -2 from bulbs of genus Tulipa.

A;Reference number: JE0183; MUID:98357241; PMID:9692212
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C;Species: Conus tulipa (tulip cone)
C;Species: Conus tulipa (tulip cone)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 15-Sep-2000
C;Accession: JC7335
R;Yamagami, T.; Tsutsumi, K.; Ishiguro, M.
Biosci. Biotechnol. Biocchem. 64, 1394-1401, 2000
A;Title: Cloning, sequencing, and expression of the tulip bulb chitinase-1 cDNA.
A;Reference number: JC7335
   DB 2;
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      Score 8; DB 2; ; Pred. No. 20; 0; Mismatches
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0.9%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches
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      100.0%;
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   Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                   142 LIKKGDAA 149
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                                                                                                                                       143 LIKKGDAA 150
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AG2987
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Agrobacterium tumefaciens
C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C; Accession: E98296
C; Accession: E98296
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Ascience 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Status: DF011minary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-262 <COL>
A;Residues: 1-262 <COL>
A;Cross-references: GB:Z79701; GB:AL123456; NID:g3261635; PIDN:CAB02028.1; PID:e264143;
C;Genetics: strain H37Rv
A;Gene: Rv1514c
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Aftile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Attle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Accession: AC2987

A;Accession: preliminary

A;Accession: preliminary

A;Accession: Lype: DMA

A;Readues: 1-270 < XUR>
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-270 < KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89895.1; PID:g15159842; GSPDB:GN00170
C;Genetics:
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A;Experimental source: strain C58 (Dupont)
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100.0%; Pred. No. 20;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches
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A;Map positIon: linear chromosome
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Matches 8, Conservative
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368 IALLVAGV 375
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Best Local Similarity
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A,Molecule type: DNA
A,Residues: 1-325 <STO>
            A;Molecule type: DNA
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erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A.Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry, C.; Quail, M.; Rutherford, R.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
                                                                                                                                                        Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD3003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 <kUR>
A;Cross-references: GB:AE008689; PIDN:AAL4442.1; PID:g17742043; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: accA
A;Map position: linear chromosome
C;Superfamily: acetyl-CoA carboxyltransferase alpha chain
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A;Map position: linear chromosome
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
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100.0%; Pred. No. 23;
tive 0; Mismatches
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Best Local Similarity 100.
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C,Accession: C87464
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, K.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Fitle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
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C,Accession: B95914
E,Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A,Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A,Reference number: A95842; MUID:21396508; PMID:11481431
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A; Status: preliminary
A; Accession: B99914
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-33 «KUR>
A; Cross-references: GB: AL591985; PIDN: CAC48981.1; PID: g15140466; GSPDB: GN00167
A; Experimental source: strain. D121, meapplasmid pSymB
A; Experimental source: strain. D121, meapplasmid pSymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P.; Hyman, R.W.; Jones, T.
B; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K.
A; Reference number: A96039; MUD: 21368234; PMID: 11474104
A; Contents: annotation
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A;Residues: 1-321 <PAR>
A;Residues: 1-321 <PAR>
A;Croser-references: GB:AL513382; PIDN:CAD06879.1; PID:g16505527; GSPDB:GN00176
C;Genetics:
A;Gene: ycfF
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
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100.0%; Pred. No. 24;
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Best Local Similarity 100.
Matches 8; Conservative
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santhopine deaminating protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: AB3160
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Mclells, S.; Gilelt, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F.
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AyTitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; WUID:21608550; PMID:11743193
A,Accession: AB3160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE008687; PIDN:AAL45696.1; PID:g17743424; GSPDB:GN00188
A;Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 Cipate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 15-Oct-1999 #sequence_revision 1981 #seference number: 219085 #seference number: 219085 #secession: T19181 #secess
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19180
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100.0%; Pred. No. 28;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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374 GVTGLISG 381
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                                                                            15 GVTGLISG 22
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Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-380 <KUR>
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AP1434
AP1434
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AP1434
AP3-600 quinol oxidase chain II [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 03-Jun-2002
C;Accession: AF1434
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
I; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A;Authors: Kreft, J.; Simoes, N.; Tisteria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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AR1806
AR1806
AR3-600 quinol oxidase chain II [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 03-Jun-2002
C;Accession: AF1806
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C;Superfamily: bo-type ubiquinol oxidase chain II precursor; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
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C;Keywords: copper; electron transfer; membrane-associated complex; respiratory chain
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A;Cross-references: GB:NC_003210; PIDN:CAC98228.1; PID:g16409372; GSPDB:GN00177
A;Experimental source: strain EGD-e
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A,Residues: 1-368 <GLA>
A,Cross-references: GB:AL592022; PIDN:CAC95246.1; PID:g16412434; GSPDB:GN00178
A,Experimental source: strain Clip11262
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                                          Length 353;
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                                          DB 2;
                                      0.9%; Score 8; DB 2
100.0%; Pred. No. 26;
iive 0; Mismatches
                                 Query Match 0.9
Best Local Similarity 100.
Matches 8; Conservative
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A; Status: preliminary
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A;Molecule type: DNA
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A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A,Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0826
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-443 <PAR>
A;Coss_references: GB:AL513382; PIDN:CAD02761.1; PID:g16503771; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wypotherical protein trp6 [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C84306
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H., Alam, M.; Feritas, T. 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows R;Barnett, M.J.; Fisher, R.F.; Jones, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9988, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A55262, MUID:21396509; PMID:11481432
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Cross-references: GB:AE006469; PIDN:AAK65522.1; PID:g14523997; GSPDB:GN00165
A;Cross-references: GB:AE006469; PIDN:AAK65522.1; PID:g14523997; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSyma
A;Experimental source: strain 1021, megaplasmid pSyma
B;Galibert, F.; Finan, T.M.; Long, S.R.; Puneler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
C.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H95369
EglC ENDO-1,3-1,4-BETA-GLYCANASE (EC 3.2.1.-) [imported] - Sinorhizobium meliloti (strai C,Species: Sinorhizobium meliloti
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE004437; NID: 910581015; PIDN: AAG19815.1; GSPDB: GN00138
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.00.0%; Pred. No. 32;
.ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                          A,Gene: STY2805
C,Superfamily: L-lysine transport protein
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LGTALAGI 138
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A;Molecule type: DNA
A;Residues: 1-447 <STO>
                                                                                                                                                                                                                                                                                                      STY2805
                                                                                                                                                                                                                                                                   C:Genetics:
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G4422
GTP-binding protein obg - Mycoplasma genitalium
C; Species: Mycoplasma genitalium
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 19-Jan-2001
C; Accession: E6424
R; Fraser, C. M.; Gocayne, J. D.; White, O.; Adams, M. D.; Clayton, R. A.; Fleischmann, R. D.;
N.; Fraser, C. M.; Gocayne, J. D.; White, O.; Adams, M. D.; Clayton, R. A.; Fleischmann, J. C.
Science 270, 397-403, 1995
A; Filerence number: A6420; MUID:96026346; PMID:756993
A; Reference number: A64200; MUID:96026346; PMID:91046095; TIGR:MG384
A; Residues: 1-433 -TIGR>
A; Residues: 1-137 -TIOOP
C; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Genetics
C; Reywords: GTP binding protein obg; translation elongation factor Tu homology
C; Keywords: GTP binding #status predicted
F; 189-194/Region: GTP-binding #status predicted
F; 182-215/Region: GTP-binding #status predicted
F; 212-215/Region: GTP-binding #status predicted
F; 212-215/Region: GTP-binding #status predicted
F; 309-313/Region: GTP-binding #status predicted
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probable cadaverine/lysine antiporter [imported] - Salmonella enterica subsp. enterica scrovar Typhi
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AE0826
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
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       R;Matthews, P.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19085
A;Accession: T19180
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-399 «ML>
A;Cross-references: EMBL:Z68214; PIDN:CAA92445.1; GSPDB:GN00022; CESP:C10C5.3
A;Experimental source: clone C10C5
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A,Introns: 27/1; 48/3; 215/3; 268/1; 303/3; 330/2; 350/3; 383/1
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100.0%; Pred. No. 29;
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 ADELGIAR 55
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Matches 8; Conserva
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A; Experimental source: serotype a; strain RM107; ATCC 9006
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|S AAVGSAVG 22
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                                                                                                                                                                                                                              69 SKLDFSKV 76
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A;Residues: 1-477 <STO>
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 0.2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84372
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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CDP-ribitol pyrophosphorylase - Haemophilus influenzae

C;Species Haemophilus influenzae

C;Species Haemophilus influenzae

C;Species Haemophilus influenzae

C;Date: 27-Apr-1996 #sequence revision 17-May-1996 #text_change 08-Oct-1999

C;Accession: S60902; S49238; $44071

C;Accession: S60902; A9238; $44071

Microbiol. 15, 107-118, 1995

A;Title: Region II of the Haemophilus influenzae type b capsulation locus is involved in A;Reference number: S60902; MUID:95272382; PMID:7752885

A;Reference number: S60902
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A; Experimental source: serotype b; strain RM135
A; Note: the nuclectide sequence was submitted to the EMBL Data Library, April 1994
A; Note: the mucleotide sequence was submitted to the EMBL Data Library, September 1994
A; Description: Genetic analysis of the region II of the Haemophilus influenzae serotype A; Reference number: S49238
A; Accession: S49238
A; Accession: S49238
A; Molecule type: DNA
A; Residues: 1,'L',3-14,'I',16-39,'IF',42-70,'AG',73-101,'R',103-212,'F',214-272.'V'.274-
     Χ.
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A;Cross-references: EMBL:237516; NID:g547510; PIDN:CAAB5750.1; PID:g547511
     hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation
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A;Residues: 1-469 <STO>
A;Crose-references: GB:AE004437; NID:g10581629; PIDN:AAG20342.1; GSPDB:GN00138
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A;Molecule type: DNA
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100.0%; Pre
                                                                                                                                                 A,Gene: eglC
A,Genome: plasmid
C,Keywords: glycosidase; hydrolase
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nes 8; Conservative
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Gispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Halobacterium sp. NRC-1
Cispecies: Perb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
Cispecies: D84306
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S., Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liê
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c A;Reference number: A83550; MUID:20512582; PMID:11058132
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A;Experimental source: strain C-125
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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	Q46435 chlamydia m P10561 chlamydia t P19910 serratia ma P74142 synechocyt	P75294 mycoplasma P37511 bacillus su	Q59174 brucella me P12242 mus musculu	P04633 rattus norv Q9y2u2 homo sapien	Q46257 chlamydia p Q8nsl2 corynebacte	P38747 saccharomyc P36184 entamoeba h	P39413 drosophila	P29632 amblyornis P29633 ampelion st	P29635 colaptes ru	P29638 parus inorn P29640 ptiloprora	P29641 scytalopus	P29642 thripophaga O67185 aquifex aeo	P52693 synechococc	Q871f8 vibrio para	Q8dcf6 vibrio vuln	P00479 escherichia	PU84ZO BALMONELLA O9tlv2 cvanidium c	escherichi	P52836 flaveria ch	Q8zb39 yersinid pe Q07835 bacillus su	P52835 flaveria bi	P43/12 naemopnilus P12257 hordeum vul	043749 homo sapien	Q9x5p2 streptomyce O9cdv3 lactococcus	P59530 mus musculu	Qybras nomo sapien P55140 escherichia	Q12094 saccharomyc			P44997 naemopnilus O66403 aquifex aeo	P30759 xenopus lae	Q9kpf9 vibrio chol	Q9ajg9 vibrio prot	P52662 erwinia chr	Q13829 homo sapien	Posy4/ Baccharomyc P94463 bacillus su	Q8rdm3 fusobacteri		arabidopsi	Q8m9x2 chaetosphae		bacil	Q8cwwww streptococc O14734 homo sapien	oryza	002467 spodoptera P58137 mus musculu	escherichi	אספילא פכוודיספטרכיי
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                                                                       nycoplasma
                                                                                                                                                                                  rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=J96 / Serotype O4;
MEDLINE=85234404; PubMed=3891743;
Felmlee T., Pellett S., Welch R.A.;
"Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
J. Bacteriol. 163:94-105(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANBOUGS: The hemolygin of E.coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=85258115; PubMed=3894051; Nicaud J.-M., Mackman N., Gray L., Holland I.B.; Nicaud J.-M., Mackman N., Gray L., Holland I.B.; Characterisation of HlyC and mechanism of activation and secretion of haemolysin from E. coli 2001."; FEBS Lett. 187:339-344(1985).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.

DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.

DOWAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin.

PIM: Palmitoylated by hlyC. The toxin only becomes active when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                P47793 | P26189 | O02754 | Q8kcq3 (Q829Y8 ) O34472 | P43931 | P63931 | Q60739 | Q8y7b6 | D8y7b6 | D8y7
P76349
P14997
P03094
O32861
                                                                                        Q8p8w5
Q97w02
Q57511
P72183
O68547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the urinary tract.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                WN4A_BRARE
ADA_SALTY
CEBA_BOVIN
                                                                                                          DP42_SULSO
FLIM_BORBU
HEMZ_PROFR
LPCC_RHILV
                                                                                                                                                                                                                                                                                                                    BACSU
                                                                                          XANCP
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    Hemolysin, chromosomal
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Hess J., Wels W., Vogel M., Goebel W.;
"Nucleotide sequence of a plasmid-encoded hemolysin determinant and
"Nucleotide sequence of a plasmid encoded hemolysin sequence.";
its comparison with a corresponding chromosomal hemolysin sequence.";
FEMS Microbiol. Lett. 34:1-11(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE-95099325; PubMed-7801126;
Stanley P., Packman L.C., Koronakis V., Hughes C.;
"Fatty acylation of two internal lysine residues required for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid Inc12 pHLY152.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                         Pfam; PF00353; hemolysinCabind; 6.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR00488; RTXTOXINA.
Hemolysis; PS00330; HEMOLYSIN CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprocein; Palmitate.
POTENTIAL.
TRANSMEM 237 259 POTENTIAL.
TRANSMEM 364 410 POTENTIAL.
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89 PALMITATE (BY SIMILARITY).
6 A -> T (IN STRAIN 2001).
109867 MW; 196D5C0A9A28B54D CRC64;
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16 X REPEATS, GLY-RICH.
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01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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0; Mismatches
or send an email to license@isb-sib.ch)
                    EMBL, M10133, AAA23975.1; -.
EMBL, X02768; CAA26546.1; -.
PIR, A24433; LEECA.
InterPro, IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: The hemolysin of E.Coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.

DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                J. Bacteriol. 178:5422-5430(1996).
-1- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                          activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin.

PIM: Palmitoylated by hlyC. The toxin only becomes active when
                                                                       Ludwig A., Garcia F., Bauer S., Jarchau T., Benz R., Hoppe J., Goebel W.;
"Analysis of the in vivo activation of hemolysin (HlyA) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00353; hemolyginCabind; 6.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate; Plasmid.
                                                                                                                                                                                                                                                                                                                                                  the urinary tract.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14; DB 1; Length 1024;
Pred. No. 2.2e-05;
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16 X REPEATS, GLY-RICH.
toxic activity of Escherichia coli hemolysin."; Science 266:1992-1996(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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PALMITATE.
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                                          PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE=96404790; Pubmed=8808931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M14107; AAA98233.1; -.
InterPro; IPR001343; Hemlyen_Ca_bind.
InterPro; IPR003995; RtxA.
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                                                                                                                      Escherichia coli."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lipoprotein; P
TRANSMEM 23
TRANSMEM 26
TRANSMEM 36
DOMAIN 72
                                                                                                                                                                                 defined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The deficient of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: characterization of the ApxIII operons.";

The ct. Immun. 62:4411-4418(1994).

Infect. Immun. 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jansen R., Briaire J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-Seroctype 2;
MEDLINE-92263992; PubWed=8494611;
Chang Y.-F., Shi J., Ma D.-P., Shin S.J., Lein D.H.;
"Molecular analysis of the Actinobacillus pleuropneumoniae RTX toxin-III gene cluster.";
DNA Cell Biol. 12:351-362(1993).
                                                                                                                                                                                                                    Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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POTENTIAL.
11 X REPEATS, GLY-RICH.
1.
        PRT; 1049 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L12145; AAA21924.1; -... EMBL; X8005c, CAB37652.1; ALT_SBQ. PIR, S51784; S51784; LINTEPPO; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003995; RtxA. Ffam; PF00353; hemolysinCabind; 6... Pfam; PF02382; RTX; 1...
                                                                                                                                                                  IIIA) (CLY-IIIA).
APXIIIA OR CLYIIIA OR RTXA OR PTXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=1536 / Serotype 2;
MEDLINE=95012630; PubMed=7927703;
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PRINTS; PR01488; RTXTOXINA.
        STANDARD;
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331
413
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RT31 ACTPL
P55130;
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REPEAT
REPEAT
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14; Conservative

Matches

Local Similarity

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Gaps

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0; Indels

100.0%; Pred. No. 2.2 tive 0; Mismatches

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TRANSMEM
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STRAIN=Serotype 8:
MEDLINE=93162836; pubMed=8412615;
MEDLINE=93162836; pubMed=8412615;
MADLINE=93162836; pubMed=8412615;
MEDLINE=93162836; pubMed=8412615;
MEDLINE=93162836; pubMed=8412615;
MEDLINE=93162836; pubMed=8412615;
MEDLINE=93162836; pubMed=8412615;
MEDLINE
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                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jansen R., Briaire J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTX-III toxin determinant A from serotype 8 (APX-IIIA) (Cytolysin
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APXIIIA OR CLYIIIA OR RTXA OR PTXA.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                Length 1049;
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                112491 MW; F99846BFD4E5CE72 CRC64;
                                                                                                                                                                                                                                                           Score 14; DB 1; Le
; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1052 AA
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MEDLINE=95012630; PubMed=7927703;
                                                                                                                                                                                                                                                                                    100.0%; Pr
                      EMBL; X80055; CAA56358.1; -. EMBL; X68815; CAA48711.1; -.
                                                                                                                                                                                                                                                                     1.5%;
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                                                                                                                                                                                                                                                                                                                    Conservative
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                      785
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nes 14; Conserv
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     7711
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P55131;
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Matches
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Infect. Immun. 60:2166-2173 (1992).
Infect. Immun. 60:2166-2173 (1992).
-!- PUNCTION: One of the virulence factors of A.suis might be a secreted cytotoxin, possibly the extracellular hemolysin.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
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-!- PTM: Palmitcylated by liktc. The toxin only becomes active when modified (By similarity).
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the cytotoxin (By similarity)
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DOMAIN: The three transmembrane domains are believed to be
                                                                                                                PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PR0148B; RTXTOXINA.
PROSTITE; PS00330; HEMOLYSIN CALCIUM; 3.
TOXIN; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burrows L.L., Lo R.Y.; "Molecular characterization of an RTX toxin determinant from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 1; Length 1052;
Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
08-REB-2003 (Rel. 41, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA) (CYTC) (APPA).
APPA OR CLYIIA OR HLYIIA OR CYTC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112809 MW; F83AFE25A6FD8758 CRC64;
                                                                                                                                                                                                                                                                                                                                                       GLY-RICH
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                                                                                                                                                                                                                                                                                                                                                       7 X REPEATS,
                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL. POTENTIAL.
InterPro, IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
                                                      Pfam; PF00353; hemolysinCabind; 6. Pfam; PF02382; RTX; 1.
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Matches 14; Conservative
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Q00951;
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ACTPL
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P55128;
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REPEAT
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: One of the virulence factors of A.pleuropneumoniae, which shows a weak hemolytic activity and is moderately cytotoxic for alveolar macrophages and neutrophils.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang Y.-F., Young R., Struck D.K.; "Cloning and characterization of a hemolysin gene from Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
RTX-II toxin determinant A (APX-IIA) (Hemolysin IIA) (HLY-IIA)
(Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellales; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cytolysins of Actinobacillus pleuropneumoniae serotype 9.";
                                                                                                                                                                       PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROSTE; PS00330; HEMOLYSIN_CALCIUM; 1.
HemOLY94; TOXIN; CYCOLY9515; Repeat; Calcium; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11; DB 1; Length 956; Pred. No. 0.023; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smits M.A., Briaire J., Jansen R., Smith H.E., Kamp E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102453 MW; 3415FF1D7ADD4365 CRC64;
                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
9 X REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    956 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Isolate CVI 13261 / Serotype 9;
MEDLINE=92040145; PubMed=1937809;
                                                                      EMBL; M90440; AAA21918.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PP00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Haemophilus) pleuropneumoniae.";
DNA 8:635-647(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Serotype 5;
MEDLINE=90126233; PubMed=2693022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.2%; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392 ALLVAGVTGLI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369 ALLVAGVTGLI 379
                                                                                                                                                                                                                                                      Palmitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794
956 AA;
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                                                                                                                                                                                                                                                    Lipoprotein; F
TRANSMEM 23
TRANSMEM 30
TRANSMEM 38
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ID RT2A_ACTPL
AC P15377;
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calcium, which is required for target cell-binding or cytolytic activity (By similarity).

-!-DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).

-!-PTM: Palmicoylated by apxIIC. The toxin only becomes active when modified (By similarity).

-!-SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amortation update)
RTX-I toxin determinant A from serotypes 1/9 (APX-IA) (Hemolysin IA) (HY-IA) (Cytolysin IA) (CLX-IA).
APXIA OR CLYIA OR HIYIA.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frey J., Meier R., Gygi D., Nicolet J.; "Nucleotide sequence of the hemolysin I gene from Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0313; CAENDNGRPT.
PRINTS; PRO14488; RTXTOXINA.
PROSITE; PS00310; HEWOLYSIN CALCIUM; 1.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102531 MW; BDBCABBADF14A641 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M30602; AAA87232.1; -.
EMBL; K3111; CAA43423.1; -.
PIR; B33389; B33389.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PP00353; hemolysinGabind; 5.
Pfam; PP02382; RTX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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Infect. Immun. 59:3026-3032(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S 4074 / Serotype 1;
MEDLINE=91348845; PubMed=1879928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity luv.
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 ALLVAGVTGLI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLVAGVTGLI 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein; I
TRANSMEM 2:
TRANSMEM 20
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CONFLICT
CONFLICT
SEQUENCE
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CONFLICT
CONFLICT
                                                                                                             Query Match
REPEAT
REPEAT
                                                                                                                                                                                                                                      RT12 ACTPL
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                                                                                                                      STRAIN=ISOLATE CVI 13261 / Serotype 9;
MEDLINE=93366425; PubMed=8359891;
Jansen R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
"Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin
                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                Frey J., Haldimann A., Nicolet J., Boffini A., Prentki P.; "Sequence analysis and transcription of the apxI operon (hemolysin I) from Actinobacillus pleuropneumoniae."; Gene 142:97-102(1994).
                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=S 4074 / Serotype 1;

Chang Y., Ann N.;

Chang Y., Chin N.;

Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: One of the virulence factors of A.pleuropneumoniae,
which has a strong hemolytic activity and is cytotoxic for
alveolar macrophages and neutrophils.

-I- SUBCELLULAR LOCATION: Secreted.

-I- DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                     activity.

-!- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).

-!- FTM: Palmitoylated by apxIC. The toxin only becomes active when modified (By similarity).

-!- MISCELIANEOUS: ApxIA is partially deleted in serotypes 2, 4, 6, 8, 12, and totally deleted in serotype 3.

-!- MISCELIANEOUS: The sequence shown is that of serotype 1.

-!- MISCELIANEOUS: The sequence shown is that of serotype 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E EMBL; X52899; CAA48586.1; -.
R EMBL; X52899; CAA48586.1; -.
R EMBL; X31317; CAA51548.1; -.
R EMBL; U05042; AAB05034.1; -.
R EMBL; U05042; AB005034.1; -.
R EMBL; U05042; AB001343; Hemlysn_Ca_bind.
R InterPro; IPR001343; Hemlysn_Ca_bind.
R Pfam; PF00353; hemolysinCabind; 6.
R Pfam; PF00353; CABNDNGRPT.
R PRINTS; PR004818; RTX; 1
R PRINTS; PR004818; RTX; 1
R PRINTS; PR014818; REMOLYSIN_CALCIUM; 2.
R PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
R HEMOLYSIS; TOXIN, CALCIUM; 2.
R HEMOLYSIS; TOXIN, CALCIUM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 X REPEATS, GLY-RICH
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         SEQUENCE FROM N.A.
STRAIN=S 4074 / Serotype 1;
MEDLINE=94237497; PubMed=181764;
                                                                                                                                                                            I (ApxI) operon.";
Infect. Immun. 61:3688-3695(1993)
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TRANSMEM 226 256
                                                                                                             SEQUENCE FROM N.A.
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REPEAT
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FZB-2003 (Rel. 41, Last annotation update)
RTX-I toxin determinant A from serotypes 5/10 (APX-IA) (Hemolysin IA)
APXIA OR CLYIA OR HLYIA.
                                                                                                                                                                                                                                             Gaps
                                                                  REF. 3 AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity.

-!- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).
-!- PTM: PALMITOYLATED BY ARXIC. The toxin only becomes active when modified (By similarity).
-!- MISCELLANEOUS: APXIA is partially deleted in serotypes 2, 4, 6, 8, 12, and totally deleted in serotype 3.
-!- MISCELLANEOUS: The sequence shown is that of serotype 10.
-!- SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=13039 / Serotype 10;
MEDLINE=94276858; PubMed=8007819;
Magal S., Yagihashi T., Ishihama A.;
"DNA sequence analysis of an allelic variant of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxIA) from serotype 10.";
Microb. Pathog. 15:485-495(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chin N., Frey J., Chang C.F., Chang Y.F.; "Identification of a locus involved in the utilization of iron by
                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                             1.2%; Score 11; DB 1; Length 1023; 100.0%; Pred. No. 0.024; ve 0; Mismatches 0; Indels
11.
12.
13.
AMPYLTLA -> GNALSNTR (IN REF. R -> A (IN REF. 3 AND 4).
Q -> E (IN REF. 3 AND 4).
TC -> R (IN REF. 3 AND 4).
17 -> R (IN REF. 3 AND 4).
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FEMS Microbiol. Lett. 143:1-6(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K17 / Serotype 5;
MEDLINE=96401417; PubMed=8807793;
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                                                                                                                                                                                                                         100.08;
                                                                                                                                                         110193
                                                                                                                                                                                                                      Local Similarity 100 tes 11; Conservative
                                                                                                                                                                                                                                                                                         266 AQRVAAGLSTT 276
                                                                                                                                                                                                                                                                                                                                  289 AQRVAAGLSTT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
    827
836
845
217
374
562
688
  822 82
831 83
840 84
210 21
374 37
562 56
687 68
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P55129;
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Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene from a Pasteurella
haemolytica-like organism, encoding a new member of the RTX toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMPYLTLA -> GNALSNTR (IN REF. 2).
E -> Q (IN REF. 2).
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PRINTS; PR01488; RTXTOXINA.
PROSTIE; PS00330; HEMOLYSIN CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11; DB 1; Length 1023;
Pred. No. 0.024;
0; Mismatches 0; Indels
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-> L (IN REF. 2).
183C7C15EE57DB55 CRC64;
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POTENTIAL.
13 X REPEATS, GLY-RICH.
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                     EMBL; D16582; BAA04014.1; -.
EMBL; U04954; AAB17220.1; -.
EMBL; V33116; CAA51546.1; -.
PIR; 139641; 139641.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 6.
Pfam; PF02392; RTX; 1.
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1023 AA;
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Best Local Similarity
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01-OCT-1996
28-FEB-2003
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P55123;
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FUNCTION: Virulence factor which is cytotoxic for leukocytes but
                              is not hemolytic.
--- SUBCELLIARA LOCATION: Secreted.
--- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                            involved in pore formation by the cytotoxin (By similarity).

1. PTM: PalmitoViated by lktC. The toxin only becomes active when modified (By similarity).
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0
                                                                                                                                                    activity.
-!- DOWAIN: The three transmembrane domains are believed to be
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L12148; AAA16444.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Interprotein; Palmitate.
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MEDLINE=87306837; PubMed=3040588;
Lo R.Y.C., Strathdee C.A., Shewen P.E.;
"Nucleotide sequence of the leukotoxin genes of Pasteurella
                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1%; Score 10; DB 1; Length 947;
100.0%; Pred. No. 0.23;
ive 0; Mismatches 0; Indels
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LKAI PASHA
SIAU...
LKAI PASHA
PIG535;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
....-2003 (Rel. 41, Last annotation update)
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Best Local Similarity 100.
Matches 10; Conservative
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(Rel. 34, Last sequence update) (Rel. 41, Last annotation update)

953 AA.

STANDARD;

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                                                                                                                                                                                                                                                                                                                 STRAIN-Serotype T3;
MEDLINE=94041617; PubMed=8225575;
MEDLINE=94041617: PubMed=8225575;
MOICCULAR TAILY OF R.Y.C., Olah-Winfield E.;
Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).
-i- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         defined.
--- SUBCELLULAR LOCATION: Secreted.
--- DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity.
-!- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).
-!- PTM: Palmitoylated by lktC. The toxin only becomes active when modified (By similarity).
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq.
28-PEB-2003 (Rel. 41, Last anno
                                                                                                                     Leukotoxin from serotype T3.
                                                                                                                                                                      Pasteurella haemolytica.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
LKA3 PASHA
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                                                                                                                                                                                                                                           STRAIN=Serotype A1 / PHL101;
MEDLINE=90236888; PubMed=2185213;
Highlander S.K., Engler M.J., Weinstock G.M.;
Highlander dexpression of the Pasteurella haemolytica Leukotoxin.";
J. Bacteriol. 172:2343-2350(11990).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted. DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).

PIM: Palmitcylated by lktC. The toxin only becomes active when modified (By similarity).

SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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6 X REPEATS, GLY-RICH (BY SIMILARITY).
                                           STRAIN=Serotype A1 / PHL101;
MEDINE=89210283; PubMed=270712;
Highlander S.K., Chidambaram M., Engler M.J., Weinstock G.M.;
"DNA sequence of the Pasteurella haemolytica leukotoxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00313; CÁBNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
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100.0%; Pred. No. 0.23;
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D -> Y (IN REF. 2).
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EMBL; M24197; AAA25543.1; -.
PTR; B30169; B30169.
InterPro: IPR001343; Hemlysn_Ca_bind.
InterPro: IPR003995; RtxA.
Pfam; PP00353; hemclysinCabind; 5.
Pfam; PP02382; RTX; 1.
                                                                                                                                                                                                                       SEQUENCE OF 884-953 FROM N.A.
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953 AA;
                                                                                                                                                                         DNA 8:15-28(1989).
[2]
SEOUENCE FROM N.A.
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                                                                                                PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            101948 MW; FDBDCE2FDC85FDF2 CRC64;
                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
6 X REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 10; DB 1;
100.0%; Pred. No. 0.23;
tive 0; Mismatches
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EMBL; U01216; AAB36691.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001995; RtxA.
                                                              Pfam; PF00353; hemolysinCabind; 5. Pfam; PF02382; RTX; 1.
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Best Local Similarity 100.
Matches 10; Conservative
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TRANSMEM
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RESULT 12 LKAB_PASHA

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Gaps

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0; Indels

10; Conservative 265 LAQRVAAGLS 274 283 LAQRVAAGLS 292

Matches

6 g LKA3_PASHA

RESULT 11

Local Similarity

955 AA

STANDARD;

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SEQUENCE FROM N.A.
STRAIN=Serotype T10;
MEDLINE=96425875; PubMed=8828217;
Lainson F.A., Murray J., Davies R.C., Donachie W.;
"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica serotype Al leukotoxin.";
Microbiology 142:2499-2507(1996).
-i- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                       DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                    activity.
-!- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).
-!- PTM: Palmitoylated by lktC. The toxin only becomes active when MODIFIED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBL_TaxID=75985;
                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
                                                                       Leukotoxin from serotype T10
                                                                                                   Pasteurella haemolytica
LKAA PASHA
P55117;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                      STRAIN=Serotype Ail;
MEDLINE=94041617; PubMed=8225575;
MEDLINE=94041617; PubMed=8225575;
Burrows L.L., Olah-Winfield E., Lo R.Y.C.;
"Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).
-i- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                       DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                    activity.

DOWAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY). PTM: Palmitoylated by ltt. The toxin only becomes active when modified (By similarity). SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
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                           (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
    953 AA
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ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
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InterPro; IPR003995; RtxA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
                                                                         Leukotoxin from serotype All
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Best Local Similarity 100.
Matches 10; Conservative
   STANDARD;
                                                                                                   Pasteurella haemolytica
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761
770
779
7953 AA;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                               NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein;
                            01-OCT-1996
                                          01-OCT-1996
28-FEB-2003
   LKAB PASHA
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DOMAIN
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                                                                   ong as its content is in no way noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                            the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
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Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 955; 0.23;
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                                                                                                                 entities requires a license agreement (S.
or send an email to license@isb-sib.ch).
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Pred. No.
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
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                                                                                                                                                                                   EMBL; Z26247; CAA81206.1; -.
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PRINTS; PR01488; RTXTOXINA.
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FRANSMEM
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Gaps

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0.23;

RESULT 13 LKAA_PASHA

RESULT 14

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                                                                                                                                                                                                                                    MEDLINE-21173699; PubMed=11259647;
MEDLINE-21173699; PubMed=11259647;
Micraman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-:- FUNCTION: Synthesis of alpha-(+)-lipoic acid. It may be involved in the sulfur insertion chemistry in lipoate biosynthesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Lipoate biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 90 IRON-SULFUR (POTENTIAL).
94 94 IRON-SULFUR (POTENTIAL).
97 97 IRON-SULFUR (POTENTIAL).
325 AA, 36161 MW, 2A1606CD9C3B6400 CRC64;
28-FEB-2003 (Rel. 41, Last sequence update)
Liperseperson (Rel. 41, Last annotation update)
Liperseperson acid synthetase (Lip-syn) (Lipeate synthase)
LIPA OR CC1735.
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16-OCT-2001 (Rel. 40, Last annotation update)
Probable GTP-binding protein MG384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.9%; Score 8; DB 1
100.0%; Pred. No. 9.9
ative 0; Mismatches
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HAMAP, MF 00206; -; 1.
InterPro; TPR006638; Elp3.
InterPro; IPR003699; Lipoate_synth.
Pfau, PF04055; Radical_SAM; 1.
SWART; SM0729; Elp3; 1.
TIGRFAMs; TIGR00510; lipa; 1.
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                                                                                                                                            Caulobacteraceae, Caulobacter
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PIR; C87464; C87464.
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                                                                                                    Caulobacter crescentus.
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P47624;
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STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                      MEDLINE-98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLenn J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                            Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.9%; Score 8; DB 1; Length 262;
100.0%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tuberculist, Rv1514c; -
InterPro, IPR001173; Glyco_trans_2.
Pfam; PF00555; Glycos transf_2; 1.
Hypothetical protein; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 AA; 28965 MW; 6B29BF8D31923E75 CRC64;
                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
8-FEB-2003 (Rel. 41, Last annotation update)
Putative glycosyl transferase Rv1514c (EC 2.-.-).
RV1514C OR MT1564 OR MTCY277.36C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AA
                           262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE007023; AAK45831.1; -.
PIR; E70714; E70714.
TIGR; MT1564; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPA CAUCR STANDARD;
Q9A7Ī8;
28-FEB-2003 (Rel. 41, Created)
                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      746 DGGSGDDV 753
                                                                        01-NOV-1997 (Rel. 35,
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                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE 262 AA;
                                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
                         YF14 MYCTU
P71793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bishai W.;
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RESULT 15 LIPA_CAUCR

Matches

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Length 325; 0; Indels

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Complete proteome.
                        FROM N.A.
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P38112;
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CONFLICT
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MAKS YEAST

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              SECUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; Dubded-756993;

Fraser C.M., Gocayre J.D., White O., Adams M.D., Clayton R.A.,

Pleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Pleischmann B.D., Weidmann J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).

-! SIMILARITY: Belongs to the GTP1 / OBG family.
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Sharypova L.A., Yurgel S.N., Keller M., Simarov B.V., Puehler A.,
Becker A.;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Endo-1,3-1,4-beta-1ycanase eglC (EC 3.2.1.-) (Succinoglycan biosynthesis protein eglC)
EGLC OR RA0864 OR SMA1587.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPRO06074; GTP1/OBG dom.
InterPro; IPRO06073; GTP1_OBG.
InterPro; IPRO06073; GTP1_OBG.
InterPro; IPRO060225; Small_GTP.
InterPro; IPRO06225; Small_GTP.
InterPro; IPRO06225; Small_GTP.
InterPro; IPRO06225; Small_GTP.
InterPro; IPRO0625; GTP108G.
ITGRFAMS, TIGRO025; GTP108G.
ITGRFAMS, TIGRO065; GTP1 OBG; I.
Hypothetical protein; GTP-binding; Complete proteome.
INP BIND 166 173 GTP (BY SIMILARITY).
INP BIND 212 216 GTP (BY SIMILARITY).
SEQUENCE 433 AA; 48166 MW; 08BFC7BC794BC3BE CRC64;
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100.0%; Pred. No. 13;
vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 KLEKFLOK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLEKFLOK 97
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Barnett M.J. Fisher R.F., Jones T., Komp C., Abola A.P.,

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Roch K.-C., Davis R.W., Federspiel N.A., Long S.R.;

Ralman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm M.D.C., Peck M.C., Surzycki R., Wells D.H.,

Ralman S., Keating D.H., Palm M.C., Peck M.C., Surzycki R., Wells D.H.,

C. I- FUNCTION: CLEAVES High MOLECULAR WEIGHT SUCCINOGLYCAN

DISTRIBUTION OF SUCCINOGLYCAN BY CLEAVING NASCENT SUCCINOGLYCAN

ONLY DURING A LIMITED PERIOD AFTER ITS SYNTHESIS, PERHAPS BEPORE

IT UNDERGOES A TIME-DEPENDENT CHANGE IN ITS CONFORMATION OR

AGGREGATION STATE BY SIMILARITY).

C. I- PATHWAY: Exopolysaccharide biosynthesis.

C. I- SUBSCELLULAR LOCATION: SECRETED. PROBABLY BY A TYPE-III SECRETION

SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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PROSTIE; PS01034; GHYCOSYL HYDROL F16; FALSE NEG.
PROSTIE; PS00330; HANCOSYL CALCIUM; FALSE NEG.
Exopolysaccharide synthesis; Glycosidase; Hydrolase; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 349 NUCLEOPHILE (BY SIMILARITY).
354 354 PROTON DONOR (BY SIMILARITY).
52 1 -> T (IN REF. 1).
465 AA, 49614 MW, 12CB879AED9E6558 CRC64;
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01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
MAKS OR YBR142W OR YBR1119.
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100.0%; Pred. No. 13;
live 0; Mismatches
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InterPro; IPR001343; Hemlysm Ca_bind.
Pfam; PF00722; Glyco_hydro 16; I.
Pfam; PF00353; hemolysincabind; 3.
MEDLINE=21396509; PubMed=11481432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ225896; CAB38101.1; -. EMBL; AE007273; AAK65522.1; -. PIR; H95369; H95369.
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Matches 8; Conservative
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DOMAIN
                      disease
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STRAIN=S288C;
MEDLINE=9574325; PubMed=7754712;
MEDLINE=9574325; PubMed=7754712;
Sagulski M., Becam A.-M., Grzybowska E., Lacroute F., Migdalski A.,
Sloninski P.P., Sokolowska B., Herbert C.J.;
"The sequence of 12.5 kb from the right arm of chromosome II predicts a new N-terminal sequence for the IRA1 protein and reveals two new genes, one of which is a DEAD-box helicase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                        STRAIN-S288C;
Brian K.-D., Koetter P., Rose M., Becker J., Grey M., Li Z.,
Niegemann E., Schenk-Groeninger R., Servos J., Wehner E.,
Wolter R., Brendel M., Bauer J., Braun H., Dern K., Duesterhus S.,
Gruenbein R., Hedges D., Kiesau P., Korol S., Krems B., Proft M.,
Siegers K., Baur A., Boles E., Miosga T.,
Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
Schaaff-Gerstenschlaeger I., Zimmermann F.K.;
Submitted (Aug-1994) to the EmBL/GenBank/DDBJ databases.
-- FUNCTION: INVOLVED IN MAINTENANCE OF DSRNA KILLER PLASMID.
-- SIMILARITY: BELONGS TO THE DEAD BOX HELICASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHEA BORBU STANDARD; PRT; 864 AA.

(044737; P70857; Q44877;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 37, Last annotation update)
Chemotaxis protein cheA (EC 2.7.3.-).
CHEA OR BB0669.
Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 222 ATP (POTENTIAL).
333 336 DEAD BOX.
773 AA; 87048 MW; C4FF2FBSB04FFBF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=212;
MEDLINE=98438936; PubMed=9765799;
Trueba G.A., Old I.G., Saint-Girons I., Johnson R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB 1;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z36011; CAA85100.1; -...
EMBL, X78937; CAA5539.1; -...
HSSP; Q58081; 1HV8.
SGD; S0000346; MAK5.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
Ffam; PF00270; DEAD; 1...
Ffam; PF00271; helicase_C; 1...
SWART; SM00487; DEXC; 1...
SWART; SM00487; DEXC; 1...
FMO031TE; PS00039; DEAD_ATP_HELICASE; 1...
Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                        SEQUENCE OF 770-773 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 KAADELGI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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RI A chack chew operon in Borrella burgdorferi, the agent of Lymes and ideases.

RI Glasses Miscrobiol. 148:191-200(1997).

RE STANIAN MICC 2510 / R31.

RESINIAN MICC 2510 / R31.

RES
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                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 264:15451-15456 (1989).
--- FUNCTION: One of the virulence factors of A.actinomycetemcomitans might be a cytotoxin, possibly the membrane-bound hemolysin.
--- SUBCELLULAR LOCATION: Outer-membrane associated or secreted (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified (By similarity).
MSCELLANBOUS: Its target cell specificity is restricted to human and some non-human cells of the monomyelocytic lineage.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN PAMILY.
   (BY SIMILARITY)
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytocoxin (BY SIMILARITY).

PTM: Palmitoylated by lktC. The toxin only becomes active when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89359382, PubMed=2670940;
Lally E.T., Golub E.E., Kieba I.R., Taichman N.S., Rosenbloom J.,
Rosenbloom J.C., Gibson C.W., Demuth D.R.;
"Analysis of the Actinobacillus actinomycetemcomitans leukotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene. Delineation of unique features and comparison to homologous
                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    actinomycetemcomitans).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                  0.9%; Score 8; DB 1; Length 864;
                                                                                                                                                                                   0; Indels
                                                                                                                 C1111DE0877BE624 CRC64;
   (AUTO-)
                 L -> 1 (IN REF. 1).
S -> H (IN REF. 1).
S -> G (IN REF. 1).
L -> S (IN REF. 1).
A -> S (IN REF. 1).
S -> P (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacillus actinomycetemcomitans (Haemophilus
   PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     PRT; 1050 AA.
                                                                                                                                                            100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurellaceae; Actinobacillus
                                                                                                                     98352 MW;
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                                                                                                                                                                                   Conservative
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 51
1182
187
239
362
559
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255 ELKKLADE 262
                                                                                                                   864 AA;
                                                                                                                                                                Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Leukotoxin.
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CONFLICT
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CYAA BORBR STANDARD; PRT; 1705 AA.

057506; O05179;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rifunctional hemolypain-adenylate cyclase precursor (Cyclolysin) (ACT)
Rifunctional hemolypain-adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danchin A., Boursaux Eude C.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS ADENYLATE VYCLASE BELONGS TO A SPECIAL CLASS OF
BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAWMALIAN
CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL
                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Secreted.
DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING
CALCIUM, WHICH IS REGUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC
ACTIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: RELEASED IN A PROCESSED FORM.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ADENYLYL
CYCLASE CLASS-2 FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE RTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Betsou F., Sismeiro O., Danchin A., Guiso N.,
"Cloning and sequence of the Bordetella bronchiseptica adenylate
cyclase-hemolysin-encoding gene: comparison with the Bordetella
                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
Repeat; Calcium; Transmembrane;
                                                                                                                                                                                                                                                                                                                     0.9%; Score 8; DB 1; Length 1050;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                        114194 MW; 38DF9AA24649F662 CRC64;
                                                                      14 X REPEATS, GLY-RICH
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                           POTENTIAL.
POTENTIAL.
                           POTENTIAL.
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MEDLINE=96009899; PubMed=7557410;
                                                                                                                                                                                                                                                                                                                                  100.08;
   Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pertussis gene.";
Gene 162:165-166(1995).
 Toxin, Cyto.
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1050 A.A.;
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               Lipoprotein; E
TRANSMEM 33
TRANSMEM 40
TRANSMEM 40
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   Hemolysis;
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SEQUENCE
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Matches
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18 A.

STANDARD;

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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Proteus.
                                                                                                                01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
508 ribosomal protein L24 (Fragment).
                                                                                                 01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                       Proteus vulgaris
                                                                                                                                                                                                                                         NCBI_TaxID=585;
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                                                                RL24 PR(
P20032;
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CECA_BOMMO
                                                                                                                                                                     RPLX.
                                RESULT 22
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                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PR0353; hemolysinCabind; 17.
Pfam; PR00353; hemolysinCabind; 17.
PRINTS; PR00313; CABNDWGRPT.
PRINTS; PR00319; HEMOLYSIN CALCIUM; 5.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 5.
Lyase; CAMP biosynthesis; ATP-binding; Hemolysis; Toxin; Virulence; Whooping cough; Calcium-binding; Repeat; Lipoprotein; Palmitate.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOLYSIN (BY SIMILARITY TO E.COLI HEMOLYSIN HLYA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   982 PALMITATE (BY SIMILARITY).
AA; 177153 MW; C43B30F5886C835A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, CATALYTIC.
B, ALA/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASP/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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100.0%; Pred. No. 41;
tive 0; Mismatches
                                                                                                                                                                                                   InterPro; IPR005165; Anthrax toxA.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
                                                                                                                                                                                                                                                                                                                                                                                                              CYCLASE
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16.
17.
19.
PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                       EMBL; Z37112; CAA85481.2; -.
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Matches 8; Conservative
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1207
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1597
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DOMAIN
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NP BIND
DOMAIN
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REPEAT
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SOLITIFIE TELLE TE
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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
MEDLINE=89125589; PubMed=2464692;
Cerretto D.P., Matcheakis L.C., Kearney K.R., Vu L., Nomura M.;
Cerretto D.P., Matcheakis L.C., Kearney K.R., Vu L., Nomura M.;
"Translational regulation of the spc operon in Escherichia coli.
Identification and structural analysis of the target site for S8
represent protein.",
J. Mol. Biol. 204:309-329 (1988).
-!- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
IS INVOLVED IN THE EARLY ASSEMBLY OF THE SOS SUBUNIT. IT IS NOT
INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.
-!- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] —
SEQUENCE FROM N.A.
STRAIN=C108; TISSUE=Larval fat body;
STRAIN=694369101; PubMed=7765280;
Yamano Y., Matsumoto M., Inoue K., Kawabata T., Morishima I.;
"Cloning of cDNAs for cecropins A and B, and expression of the genes in the silkworm, Bombyx mori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 7; DB 1;
100.0%; Pred. No. 8.5;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SRP-2003 (Rel. 42, Last annotation update)
Cecropin A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005825; Ribosomal L24 26.
PROSITE; PS01108; RIBOSOMAL_L24; PARTIAL.
Ribosomal protein.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth).
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TISSUE=Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serrulatus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P46066
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P45659;
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SIGNAL
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SCX4_TITSE
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Biosci. Biotechnol. Biochem. 58:1476-1478(1994).

-!- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST
SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.

-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Highest expression in fat body and hemocytes.
Is also expressed in Malpfahian tubules and to a much lesser
extent in midgut. Not present in silk gland.
-!- SIMILARITY: BELONGS TO THE CECROPIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDILINE=96243503; MEDLINE=96243503; PubMed=8711758; Corona M., Zurita M., Possani L.D., Becerril B.; Croning and characterization of the genomic region encoding toxin IV-5 from the scorpion Tityus serrulatus Lutz and Mello.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
CECROPIN A.
AMIDATION (G-62 PROVIDE AMIDE GROUP)
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P01496; P91788;
1-JUL-1986 (Rel. 01, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Toxin IV-5 precursor (Tityuscoxin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 25; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tityus serrulatus (Brazilian scorpion)
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InterPro; IPR003254; IIP_cecropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00272; cecropin; 1.
ProDom; PD003996; IIP cecropin; 1.
PROSITE; PS00268; CECROPIN; 1.
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MEDLINE=91131623; PubMed=1993690;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D17394; BAA04217.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6762 MW;
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nes 7; Conservative
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TISSUE=Venom;
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SIGNAL
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                                                            Toxicon 20:75-76(1982).
-!- FUNCTION: Binds to sodium channels and inhibits the inactivation
-!- FUNCTION: Binds to sodium channels and inhibits the inactivation
-!- SUBCELLIALAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- TISSUE SPECIFICITY: Expressed by The Pand SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
BETA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94192827; PubMed=8143874;
Martin-Eauclaire M.-F., Ceard B., Ribeiro A.M., Diniz C.R., Rochat H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00505; Knotl; 1. Tronic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Arthropoda, Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Tityus.
Possani L.D., Martin B.M., Mochca-Morales J., Svendsen I.; "N-terminal sequence of toxin IV-5 from the venom of the scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
AMIDATION (G-78 PROVIDE AMIDE GROUP)
(POTENTIAL).
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Toxins IV/III/V precursor (TSTX-IV) (Tityustoxin IV) (Ts IV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 1; Length 80;
Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; toxin_3; 1.
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Best Local Similarity
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                                            Tytius serrulatus.
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modified and this statement is not removed.
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                                                                                                                                                                                   RESULT 27
RL24 ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                   gene."
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                                                                                                                                                                       HSSP; P46066; INRB.
InterPro; IPR003614; Knotl.
InterPro; IPR0036614; Scorpion_toxinL.
Pfam; PF00037; toxin_3; 1.
Probom; P0000908; Scorpion_toxinL; 1.
SMART; SM00505; Knotl; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor; Signal; Amidation.
NON TER 1 1
SIGNAL <1 13
 the activated channels, thereby blocking neuronal transmission.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                 AMIDATION (G-78 PROVIDE AMIDE GROUP) (POTENTIAL).
FDE437EEC1335FFC CRC64;
           SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom gland.
SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY
ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perret X.; "Molecular basis of symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 387:394-401(1997).
-!- SIMILARITY: STRONG, TO A.TUMEFACIENS TI PLASMID TRAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Próteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                     TOXIN IV.
TOXIN V (POTENTIAL).
TOXIN III (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Probable conjugal transfer protein traC.
TRAC OR Y4DT.
Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 7; DB 1;
100.0%; Pred. No. 31;
ive 0; Mismatches
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                                                                                                                                                    EMBL; S69808; AAB30413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        9025 MW;
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Best Local Similarity luv...
7; Conservative
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13
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                                                                                                                                                                PIR; S43674; NTSR4T.
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114
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TRAC_RHISN
ID _TRAC_RHISN
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MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Hayabhi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohteubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIESE.Coli; STRAIN-0157.H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=111, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfaid G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
Welch R. G., Schwarts D.C.,
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE E. Coli; FATAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                              Length 102;
                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                        EMBL; AE000070; AAB92440.1; -.
Conjugation; Plasmid.
SEQUENCE 102 AA; 10205 MW; AA378F93DD06C78B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
RPLX OR B3309 OR Z4679 OR ECS4174 OR STM3429.
                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                              0.8%; Score 7; DB 1;
100.0%; Pred. No. 38;
ive 0; Mismatches
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                               entities requires a license agreement (or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECIES-E.coli; STRAIN-K12;
MEDLINE-83220807; PubMed-6222285;
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Escherichia coli 0157:H7, and
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Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        356 SAAAVGS 362
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Interpro; IPR005824; KOW.
Interpro; IPR005646; KOW sub.
Interpro; IPR001256; Ribosomal L24.
Interpro: IPR005825; Ribosomal L24_26.
Pfam; PF00467; KOW; 1.
ProDom; PD001677; Ribosomal L24; 1.
                                                                                                                                                                                                                     Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                         481 FEDGKKV 487
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                                                                                                                                                                                                                                                                                                                         FEDGKKV 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
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ID RL24 HAEIN
AC P44362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S. Cyphimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCC1elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Floraca L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                          protein S8 in Escherichia
binding site and feedback
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cerretti D.P., Mattheakis L.C., Kearney K.R., Vu L., Nomura M.; "Translational regulation of the spc operon in Escherichia coli. Identification and structural analysis of the target site for S8 repressor protein."; J. Mol. Biol. 204:309-329(1988).
                                                                                             "Primary structure of protein L24 from the Escherichia coli
                                                                                                                                                                                                         Olins P.O., Nomura M.; "Translational regulation by ribosomal coli: structural homology between rRNA
                                                                                                                                                                                                                                                                          Nucleic Acids Res. 9:1757-1764(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=S.typhimurium;
MEDLINE=89125589; PubMed=2464692;
                                                                                                                                                                                          MEDLINE=81199003; PubMed=6262737;
                                                           MEDLINE=80092112; PubMed=391595; Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000408; AAC76334.1; -. EMBL; AE005556; AAG58430.1; -. EMBL; AP002564; BAB37597.1; -.
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EMBL; U18997; AAA58106.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M10195; AAA24050.1; -.
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                                                                                                                                                            OF 85-103 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 86-103 FROM N.A.
                                             CIES=E.coli; STRAIN=K12;
                                                                                                              ribosome.";
FEBS Lett. 108:75-80(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE008857; AAL22292
Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MASS SPECTROMETRY.
                                                                                                                                                                                                                                                       target on mRNA.
                                                                                                                                                                             SPECIES=E.coli;
                              SEQUENCE
                                                                                                                                                            SEQUENCE
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EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
-!- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND
IS INVOLVED IN THE BEALY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT
INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ERd / KW20 / ATCC 51907;

MDDLINE-95350630; Pubmed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Luu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                     Length 103;
                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                103 AA; 11185 MW; 9F4CB2EFF66FAE95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L24.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                 0.8%; Score 7; DB 1;
100.0%; Pred. No. 38;
iive 0; Mismatches
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InterPro; IPR005824; KOW.
InterPro; IPR005646; KOW sub.
InterPro; IPR001256; Ribosomal L24.
InterPro; IPR005825; Ribosomal L24_26.
SMART; SM00739; KOW; 1:
TIGRFAMS; TIGRO1079; rplX_bact; 1.
PROSITE; PS01108; RIBOSOWAL L24; 1.
Ribosomal protein; Complete proteome:
INIT_MET 0
SEQUENCE 103 AA; 11185 MW; 9F4CB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
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RL24 BUCAK
ID RL24 BUCAK
AC P46177;
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NU4M_CAICR
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-I. FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 7; DB 1; Length 103;
100.0%; Pred. No. 38;
iive 0; Mismatches 0; Indels
                                                                                               Length 103;
                                                                                                                       0; Indels
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SMART; SM00739; KOW; 1.
TIGRRAMs; TIGR01079; I.DX bact; 1.
PROSITE; PS01108; RIBOSOWĀL_L24; 1.
RIBOSOMAl protein; Complete proteome.
SEQUENCE 103 AA; 11239 MW; 0A325EF73E604850 CRC64;
Pfam; PF00467; KOW; 1.
Prodom; PD001677; Ribosomal_L24; 1.
SMART; SM0739; KOW; 1.
TIGRFAMS; TIGR01079; rplX_bact; 1.
PROSITE; PS01108; RIBOSOMMi_L24; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 103 AA; 11285 MW; 3AD4903377702F19 CRC64;
                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RPLX OR RPL24 OR PM1404.
                                                                                                DB 1;
                                                                                              0.8%; Score 7; DB 1;
100.0%; Pred. No. 38;
cive 0; Mismatches
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InterPro; IPR005646; KOW sub.
InterPro; IPR003256; Ribosomal L24.
InterPro; IPR005825; Ribosomal_L24_26.
Pfam; PF00467; KOW; 1.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
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                                                                                     Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                        Pasteurella multocida
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                                                                                                                                                 481 FEDGKKV 487
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                                                                                                                                                                       87 FEDGKKV 93
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=747;
                                                                                                                                                                                                                                     RL24 PASMU
Q9CL41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                            RESULT 29
RL24 PASMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abe R., Yamashita A., Isono K.;

"Cloning and characterization of the ribosomal protein genes in the spec operon of a prokaryotic endosymbiont of the pea aphid, Acytchosiphon kondoi.";

DNA Res. 1:103-114(1994).

-! FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Archosauria; Crocodylidae; Alligatorinae; Caiman.
NCBI_TaxID=8499;
                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                          Buchnera aphidicola (subsp. Acyrthosiphon kondoi) (Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               034076;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3) (Fragment).
MTND4 OR ND4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 AA; 11336 MW; F3553FE6418BF47C CRC64;
                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 39, Last annotation update)
50S ribosomal protein L24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.8%; Score 7; DB 1;
104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 38; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005824; KOW.
InterPro; IPR0056645; KOW sub.
InterPro; IPR0013256; Ribosomal L24.
InterPro; IPR005825; Ribosomal L24_26.
Pfam; PF00467; KOW; 1.
ProDow; PD001677; Ribosomal L24; 1.
SWART; SM00179; KOW; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR01079; rplX bact; 1.
PROSITE; PS01108; RIBOSOWAL_L24; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96051390; PubMed=7584036;
                                                                                                                                                                                                                                                                                  Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D31786; BAA06586.1; -.
                                                                                                                                                                                                                          kondoi symbiotic bacterium)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481 FEDGKKV 487
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Kurashiki;
                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=42474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion.
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RL7 NEIMA
P80716;
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RL7 NEIMA
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the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                   MEDLINE=96073446; PubMed=7476123;
Kumazawa Y., Nishida M.;
"Variations in mitochondrial tRNA gene organization of reptiles as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=N.lactamica, and N.sicca; STRAIN=NRL 8828, and NRL 30016; Spence J.M., Clark V.L.; Spence J.M., Clark V.L.; "Alterations in protein profiles associated with induction of the contact-induced enhanced invasion phenotype of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                       phylogenetic markers.";
Mol. Biol. Evol. 12:759-772(1995).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria sicca.
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AA; 12070 MW; D211FBBA07A42D83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                              EMBL, D38190; BAA07383.1; -.
InterPro; IPR001750; Oxidored q1.
Pfam; PF00061; oxidored q1.
Oxidoreductase; NAD; Ubīquinone; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILLA STANDARD, PRT; 122 AA. 09ETV2; 16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 50S ribosomal protein L7/L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1;
Pred. No. 40;
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100.0%; Pred. No. ...
0; Mismatches
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InterPro; IPR000206; Ribosomal_L12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100
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TSPLLTA 11
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[1]
SEQUENCE FROM N.A.
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MEDINDE=20175755; PubMed=10710307;
MEDINDE=20175755; PubMed=10710307;
Eisen J.A., Ketchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E.,
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Felschmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair B., Cittone H., Clark B.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup A), and
Neisseria meningitidis (serogroup B)
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                             DB 1; Length 122;
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                                                                                                                          122 AA; 12567 MW; 7A87249AAC0E2D4D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
508 ribosomal protein L7/L12
RPLL OR NMA0143 OR NMB0131.
                                                                                                                                                                          0.8%; Score 7; DB 1;
100.0%; Pred. No. 44;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 AA
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MEDLINE=20222556; PubMed=10761919;
ProDom; PD001326; Ribosomal L12; 1.
TIGRFAMS; TIGR00855; L12; 1.
Ribosomal protein.
SEQUENCE 122 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:1809-1815(2000).
                                                                                                                                                 Query Match
Best Local Similarity 10v.,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitidis Z2491.";
Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=65699, 491;
                                                                                                                                                                                                                                                                                      354 GVSAAAV 360
                                                                                                                                                                                                                                                                                                                                            32 GVSAAAV 38
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MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
MEDLINE-21470413; PubMed=11586360;
Parkhil J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fervinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AA; 12491 MW; 3C962C3A11B6F535 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
505 Inbosomal protein L7/L12.
RPL. OR YPO3748 OR Y0483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 44; Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00368; -; 1.
InterPro; IPR000206; Ribosomal_L12.
Pfam, PF00542; Ribosomal_L12; 1.
ProDom; PD001326; Ribosomal_L12; 1.
TIGRFAMS; TIGR00855; L12; 1.
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                                                                                                                                                                                                                                              EMBL; AL162752; CAB83458.1; -. EMBL; AE002371; AAF40590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:523-527(2001).
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                                                                                                                                                                                                                                                                                                              PIR; H81235; H81235.
HSSP; P02392; 1CTF.
TIGR; NMB0131; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 GVSAAAV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Q8ZAP4;
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SEQUENCE
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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Neisseriaceae; Neisseria.
NCBI_TaxID=33053;
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HAWAP; MF 00368; -; 1.

InterPro; IPR000508; Ribosomal L12.

Propom; PP004126; Ribosomal L12; 1.

Propom; PD001326; Ribosomal L12; 1.

Propom; PD001326; Ribosomal L12; 1.

Ribosomal protein; Complete proteome.

SEQUENCE 122 AA; 12530 MW; 40A0C74D6B77D69D CRC64;
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100.0%; Pred. No. 44;
ative 0; Mismatches
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28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein L7/L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.8%; Score 7; DB 1;
100.0%; Pred. No. 44;
1ve 0; Mismatches
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InterPro, IPR000206; Ribosomal L12.
Pfam; PF00542; Ribosomal L12; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                     EMBL; AJ414158; CAC93216.1; -. EMBL; AE013649; AAM84072.1; -.
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Ribosomal protein.
SEQUENCE 123 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=NRL 30015;
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Q9F5M1;
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RESULT 35
RL NEIPE RL NEIPE RL OF SEPTEM REL OF SEPTEM RESERVENCY OF SEPTEM REL OF SEPTEM RESERVENCY OF SEPTEM 
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139 ELDSLIK 145
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                                                                                          Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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H2AV_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-RROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21661879; PubMed=11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne M., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., "Hessenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPLL OR RSC3035 OR RS04722.
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.00.0%; Pred. No. 45;
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(Rel. 09, Last sequence update)
(Rel. 41, Last annotation update)
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tive 0; Mismatches
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InterPro; IPR001813; 608_ribosomal.
InterPro; IPR001206; Ribosomal_L12.
Pfam; PF00428; 608_ribosomal, 1.
Pfam; PF00428; Ribosomal, L12; 1.
ProDom; PD001326; Ribosomal_L12; 1.
TIGREAMS; TIGR00855; L12; 1.
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SEQUENCE 124 AA; 12520 MW; 271C3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burkholderiaceae; Ralstonia
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nes 7; Conservative
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                                GVSAAAV 360
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                                                                                       32 GVSAAAV 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=GMI1000;
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28-FEB-2003 (
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AC P08991;
DT 01-NOV-1988
DT 01-NOV-1988
DT 28-FBB-2003
DE H16-CDB CR H16-CDB
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RL7_RALSO
ID 784-FE
DT 28-FE

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                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of a cDNA clone coding for a sea urchin histone H2A variant related to the H2A.F/Z histone protein in vertebrates."; Nucleic Acids Res. 15:4629-4644(198).

-!- FUNCTION: VARIANT HISTONES H2A ARE SYNTHESIZED THROUGHOUT THE CELL CYCLE AND ARE VERY DIFFERENT FROM CLASSICAL S-PHASE RECULATED H2A. THE EXACT FUNCTION OF VARIANT HISTONES H2A IS NOT KNOWN.

-!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3B H3 and H4. The octamer wraps approximately 146
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                      MEDLINE=87231039; PubMed=2438657;
Ernst S.G., Miller H., Brenner C.A., Nocente-Mcgrath C., Francis S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; Nucleosome core; Nuclear protein; DNA-binding;
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MEDLINE-83221493; PubMed-6574451;
MEDLINE-83221493; PubMed-6574451;
Harvey R.D., Whiting J.A., Coles L.S., Krieg P.A., Wells J.R.E.;
HAZA.F: an extremely variant histone H2A sequence expressed in the chicken embryo.";
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100.0%; Pred. No. 45;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histone H2A variant.
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PIR; S07392; S07392.
InterPro; IPR004822; Histone_core.
InterPro; IPR004819; Histone_HZA.
Pfam; PF00125; histone; 1.
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ProDom; PD000522; Histone H2A; 1.
SMART; SM00414; H2A; 1.
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Nucleic Acids Res. 16:1113-1124(1988).
                                                                  SEQUENCE FROM N.A.
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RL20_BIFLO
   SOLUTION OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELCULAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CHICKEN EMBRYO.
-!- DIVILORNITY: Belongs to the histone H2A family.

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0
                                                    SEQUENCE FROM N.A.

MEDLINE=89160327; PubMed=2493634;
Dalton S., Robins A.J., Harvey R.P., Wells J.R.E.;
Dalton From the intron-containing chicken histone H2A.F gene is not S-phase regulated.";
Nucleic Acids Res. 17:1745-1756(1989).
-! FUNCTION: VARIANT HISTONES H2A ARE SYNTHESIZED THROUGHOUT THE CELL CYCLE AND ARE VERY DIFFERENT FROM CLASSICAL S-FHASE REGULATED H2A. THE EXACT FUNCTION OF VARIANT HISTONES H2A IS NOT KNOWN.
-! SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; X13894; CAA22094.1; ALT_SEQ.
PIK; S03282; HSGH2F.
InterPro; IPR004822; Histone_core.
InterPro; IPR0040212; Histone_HZA.
Pfam; PF00125; histone; 1.
PRINTS; PR00620; HISTONEHZA.
ProDom; PD000522; Histone_HZA.
SMART; SM00414; HZA; 1.
PROSITE; PS00046; HISTONE_HZA; 1.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding; Nultigene family; Embryo.
INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat), and Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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0.8%; Score 7; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels
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   Proc. Natl. Acad. Sci. U.S.A. 80:2819-2823(1983)
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01-AUG-1990 (Rel. 15, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
HISAFZ OR H2AZ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 ELDSLIK 145
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P17317;
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H2AZ HUMAN
   NAMES OF THE STATE OF THE STATE
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GO; GO:0005718; C:nucleosome; NAS.
GO; GO:0001677; F:DNA binding activity; NAS.
GO; GO:0007001; P:chromosome organization and biogenesis (sen. . .; NAS.
GO; GO:0006334; P:nucleosome assembly; NAS.
InterPro; IPR004822; Histone_core.
InterPro; IPR002119; Histone_HZA.
                                                                                                                                                                                                                                                                                 Jordan B.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FINCTION: VARIANT HISTONES H2A ARE SYNTHESIZED THROUGHOUT THE
CELL CYCLE AND ARE VERY DIFFERENT FROM CLASSICAL S-PHASE REGULATED
H2A. THE EXACT FUNCTION OF VARIANT HISTONES H2A IS NOT KNOWN.
-!- SUBUNIT: The nucleosome is an octamer containing two molecules
each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
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                                                                                                                                                                                                                      SPECIES=Mouse; STRAIN=C57BL/6;
Rocha D., Carrier A., Anderson E., Botcherby M., Guenet J.-L.,
SPECIES=Human;
MEDLINE=90368704; PubMed=1697587;
Hatch C.L., Bonner W.M.;
Hitch C.L., Schone HA.Z. gene. Sequence and regulation.";
J. Biol. Chem. 265:15211-15218 (1990).
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100.0%; Pred. No. 45;
/ative 0; Mismatches 0; Indels
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PRINTS; PR00620; HISTONEH2A.
ProDom; PD000522; Histone_H2A; 1.
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EMBL; M37583; AAA35984.1; --
EMBL; L10138, AAC61625.1; --
EMBL; X52316; CAA36552.1; --
EMBL; X52318; CAA36554.1; --
EMBL; M37585; AAA30566.1; --
EMBL; U70494; AAB09578.1; --
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PIR; S03642; S03642.
PIR; S03644; S03644.
PDB; IF66; 27-NOV-00.
Genew; HGNC:4741; H2AFZ.
MIM; 142763;
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7; Conservative
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                                                                                                                                                                                                                                                                                                                     "The genome sequence of Biidobacterium longum reflects its adaptation to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14427 (2002)

- I- FUNCTION: This protein binds directly to 23s ribosomal RNA and is necessary for the in vitro assembly process of the 50s ribosomal subunit. It is not involved in the protein synthesizing functions of that subunit (By similarity)

- I- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                               Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                                                                                                                                    Schell M.A., Karmirantzou M., Snei B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00937; RIBOŠOWĀL 120; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
SEQUENCE 127 AA; 14605 MW; 2EF7D5D28B7BDD99 CRC64;
                        15-SEP-2003 (Rel. 42, Last sequence update) 50S ribosomal protein L20. RPLT 00 BL1367.
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127 AA.
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Pred. No. 45;
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Interpro; IPR005812; L20.
Interpro; IPR005812; L20 bact_org.
Pfam; PF00453; Ribosomal_L20; 1.
PRINTS; PR00062; RIBOSOMALL20.
PRODom; PD002389; L20; I.
TIGRFAM8; TIGR01032; rplT_bact; 1.
 PRT;
                                                                                                                                                                                                                                       STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
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100.0%; Prev
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Best Local Similarity 100.
Matches 7; Conservative
STANDARD;
                                                                                                                         Bifidobacterium longum.
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RL20 BIFLO
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Search completed: February 17, 2004, 10:20:08 Job time : 39 secs

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Gaps ö

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Mismatches

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ENKSQKLSASDIASSLNKLVGSMAL 900
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Gyles C., "Evolution of enterohemorrhagic escherichia coli hemolysin plasmids and the locus for enterocyte effacement in Shiga toxin-producing E.
Boerlin P., Chen S., Colbourne J.K., Johnson R., De Grandis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 1.5%; Score 14; DB 2; Length 998; Local Similarity 100.0%; Pred. No. 0.00015; les 14; Conservative 0; Mismatches 0; Indels
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InterPro; IPR001343; Hemlysn_Ca_bind
InterPro; IPR003995; RtxA.
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PRINTS; PR01488; RTXTOXINA.
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98290540; PubMed=9628576;
Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
Yataudo H.C., Kubota Y., Yamaichi Y., Iida T., Yamamoto K., Honda T.,
Han C., Ohtsubo A., Kasamatsu M., Hayashi T., Kuhara S.,
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Enterobacteriaceae; Bscherichia.
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Enterobacteriaceae, Escherichia.
NCBI_TaxID=83334;
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MEDLINE-98391744; PubMed=9722640;
Burland V., Shao Y., Perna N.T., Plunkett G., Sofia H.J.,
Blattner F.R.;
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Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
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       01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=97034824; PubMed=8880480;
Schmidt H., Karch H., Sarch H.,
Enterchemolytic phenotypes and genoty[es pof Shiga Toxin-producing
Esherichia coli 0111 strain from patients with diarrhea and hemolytic-
uremic syndrome: ";
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EMBL, 794129; CAA638949.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001395; RtxA.
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STRAIN=536;
MEDLINE=22267114; PubMed=12379716;
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EMBL; AJ488511; CAD33759.1;
SEQUENCE 1024 AA; 110314 MW; 9771F0A61ECF6EEB CRC64;
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Acta Med. Blol. (Nigata) 0:0-0(2000).
EMBL, AB02930; BAA93708.1; --
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 6.
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Enterobacteriaceae, Escherichia.
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"Analysis of the EHEC hly operon and its location in the physical map of the large plasmid of enterchemorrhagic Esherichia coli 0157:H7.";
Microbiology 142:907-914(1996).
EMBL; X86087; CAA6042.1;
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PRINTS; PR01488; RIXIOXINA.
SEQUENCE 998 AA; 107058 MW; 0D3BE108C309B8B3 CRC64;
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Last annotation update)
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MEDLINE=97090409; PubMed=8936317;
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MEDLINE=95172699; PubMed=7868227;
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PRINTS; PR01488; RTXTOXINA.
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nes 14; Conservative
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Matches 14; Conservative
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EHEC-HLYA.
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EHEC-HLYA.
Escherichia coli
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SEQUENCE
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Heyberger-Meyer B., Frey J., Nicolet J., Kuhnert P.; "Identification and characterization of a new RTX toxin operon (pax)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
RIX-toxin IIA.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
                                                                                                                                                                                                                                                                                                                                                                                Pasteurella aerogenes.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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Pasteurellaceae; Actinobacillus.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS003130; HEMOLYSIN CALCIUM; 1.
SEQUENCE 1049 AA; 112308 MW; 9FAS070E48CC3127 CRC64;
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PRINTS; PR01488; RTXTOXINA.
PRO912: PS00330; HEMOLYSIN CALCIUM; 1.
SEQUENCE 1052 AA; 112862 MW; CA0E160F02101F42 CRC64;
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Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.;
Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.;
"Cloning and Sequencing of Apx IIIA from Actinobacillus
pleuropneumoiae.";
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR363383; ARK50053.1;
InterPro; IPR001393; Hemlysn_Ca_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Pasteurella aerogenes.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 106588; ABF15370.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR0013995; RtxA.
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF02382; RTX; 1.
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406 ISGILEASKQAMFE 419
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Best Local Similarity
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MBDLINE=22388214; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Bucklee E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016766; AAN82018.1; -.
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Bacteria; Proteobacteria; Gammag Enterobacteriaceae; Escherichia.
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STRAIM=CCUG 19799;

MEDLIN=22031201; PubMed=12034544;

Berthoud H., Frey J., Kuhnert P.;

"Characterization of Agx and its operon: the hemolytic RTX determinant of Actinobacillus equuli.";

Vet. Microbacillus equuli.";

Vet. Microbacillus 755-174 (2002).

EMBL; AF381184; AAM45566.1; -.

InterPro; IPR001343; Hemlysn.Ca_bind.
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MEDLINE=22031201; PubMed=12034544;

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MEDLINE=22031201; PubMed=12034544;

Berthoud H., Frey J., Kuhnert P.;

"Characterization of Aqx and its operon: the hemolytic RTX determinant of Actinobacillus equuli.";

of Actinobacillus equuli.";

Vet. Microbiol. 87:159-174 (2002).

InterPro; 1PR001343; Hemlysn_Ca_bind.

InterPro; 1PR003395; RtxA.

Pfam; PF00353; hemolysinCabind; 3.

Pfam; PF003382; RTX; 1.
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Pasteurellaceae; Actinobacillus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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100.0%; Pred. No. 0.016;
iive 0; Mismatches 0; Indels
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 1.
SEQUENCE 987 AA; 105662 MW; CC34CD62BF9B745D CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
NCBI_TaxID=715;
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                                                                                                               Query Match 1.3%; Score 12; DB 2; Length 987 Best Local Similarity 100.0%; Pred. No. 0.016; Matches 12; Conservative 0; Mismatches 0; Indels
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Pfam; PF00332; hemolysinCabind; 5.
Pfam; PF00332; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PROSTITS; PR00330; HTMOLYSIN CALCIUM; 1.
SEQUENCE 956 AA; 102495 Mw; 9F8EB14EC76628D5 CRC64;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF563361, AAK6051.1;
InterPro; IPR001343; Hemlyen_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 6.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
SEQUENCE 987 AA; 105871 MW; 35440030AB522E53 CRC64;
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Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.;
"Cloning and Sequencing of Apx IIA from Actinobacillus
pleuropneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Shin N.R., Yoo H.S.; Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.; "Cloning and Sequencing of Apx IA from Actinobacilus
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 956 AA.
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InterPro; IPR001343; Hemlysn Ca bind.
InterPro; IPR003995; RtxA.
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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MEDLINE=21101823; PubMed=11157953; Davies R.K.; Davies R.L., Whitten T.S., Selander R.K.; Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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100.0%; Pred. No. 1.6;
tive 0; Mismatches 0; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF486646; AAL93195.1; -.
          Interpro; IPR001343; """", —
Interpro; IPR006626; PbH1.
Pfam; PP00353; hemolysinCabind; 8.
SWART; SW00712; CASH; 2.
SWART; SW00710; PbH1; 8.
cconfinCE 874 AA; 90159 MW; 22487F3A445427F1 CRC64;
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889 AA; 91391 MW; 6945D3971E5410D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 91.4 kDa protein.
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100.0%; Pred. No. 1.6;
ative 0; Mismatches
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Pfam; PF00353; hemolysinCabind; 8.
Hypothetical protein.
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J. Bacteriol. 183:1394-1404(2001).
EMBL, AF314521; AAG40305.1;
InterPro; IPR001753; EnCOA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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InterPro; IPR006633;
InterPro; IPR001343;
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Matches
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Q8RMZ8
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Pseudomonadaceae; Azotobacter.
NCBI_TaxID=354;
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                          Score 11; DB 2; Length 1022;
Pred. No. 0.18;
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PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
SEQUENCE 1022 AA; 110439 MW; A68E486D335467E3 CRC64;
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Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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100.0%; Pred. No. v...
... 0; Mismatches
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                                                            Query Match
Best Local Similarity 100.
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CG5833 OR CG13132.
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CSTRAIN=PH498, and PH344;

Davies R.L., Whittam T.S., Selander R.K.;

Davies R.L., whittam T.S., Selander R.K.;

"Sequence diversity and molecular evolution of the leukotoxin (lkta) gene in bovine and ovine strains of Mannheimia (Pasteurella)

"I bacteriol. 0:0-0(201).

"B BMB1, AF314518; AAG40302.1; -..

"B EMB1, AF314518; AAG40302.1; -..

"B EMB1, AF314519; AAG40301.1; -..

"B InterPro; IPR001343; Hemlyen.Ca_bind.

"InterPro; IPR001343; Hemlyen.Ca_bind.

"B Fam; PF00353; Hemlyen.Ca_bind.

"P Fam; PF00353; RXX, 1.

"P RINTS; PR00131; CABNDNGRPT.

"P RINTS; PR0166; ENOYL COA HYDRAIASE; 1.

"P ROSITE; P800166; ENOYL COA HYDRAIASE; 1.
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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J. Bacteriol. 183:1394-1404 (2001).
EMBL; AF314516; AAG40300.1;
EMBL; AF314516; AAG40300.1;
InterPro; IPR001343; Hemly5n_Ca_bind.
InterPro; IPR00395; RtxA.
InterPro; IPR00353; hemlysinCabind; 5.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL. COA HYDRATASE; 1.
SEQUENCE 953 AA; 102230 MW; 2B686808EB370090 CRC64;
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Last annotation update)
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100.0%; Pred. No. 1.7;
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100.0%; Pred. No. 1.7;
Live 0; Mismatches
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 100.0
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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SEQUENCE FROM N.A.
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Q9EV29
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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Mannheimia glucosida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
                                                                                                                                      1.1%; Score 10; DB 2; Length 946; 100.0%; Pred. No. 1.7; tive 0; Mismatches 0; Indels
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                                                PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RIXTOXINA.
PROSTIE; PRO166; ENOYL COB HYDRATASE; 1.
SEQUENCE 946 AA: 101480 Ww. 25C077859BDC76C4 CRC64;
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PRO146; BOVYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102160 Ww; A189BF80754A7907 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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J. Bacteriol. 183:1394-1404(2001).

EMBL, AF314510; AAG40294.1;
INCEPPRO. 1PR001753; ENCOA hydrtse.

INTERPRO. 1PR001343; Hemlysn.Ca_bind.

INTERPRO. 1PR001343; Hemlysn.Ca_bind.

Pfam; PP00353; hemolysinCabind; 5.

Pfam; PF02382; RTX; 1.
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MEDLINE=21101823; PubMed=11157953;
              Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
 InterPro; IPR003995; RtxA.
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Best Local Similarity 100.
Matches 10, Conservative
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Best Local Similarity 100.
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Q9ETX2
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Q9EV31
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Matches
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Q9ETG5
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=85401;
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0; Indels
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102138 MW; C41D9EBC1D799951 CRC64;
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SEQUENCE 953 AA; 102147 MW; 11600FDA7849A1CA CRC64;
                         Created)
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EMBL, AF314514; AAG40298.1; -.
INTERPRO; IPR001753; ENCOA hydrtse.
INTERPRO; IPR001343; Hemlysn_Ca_bind.
INTERPRO; IPR0013995; RtxA.
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EMBL, AF314520, AAG40304.1.
INTECFRO, IPR001753, EMCOA hydrse.
InterPro, IPR001343; Hemlysn_Ca_bind.
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Pfam; PF02382; RTX; 1.
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PRINTS; PR01488; RTXTOXINA.
                         01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
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Matches 10; Conserv
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Q9EV25
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Davies R.L., Whitten T.S., Selander R.K.;
Sequence diversity and molecular evolution of the leukotoxin (lktA)
gene in bovine and ovine strains of Mannheimia (Pasteurella)
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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Pasteurellaceae; Mannheimia
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 A4; 101997 Ww; D593D6A577C3ADE9 CRC64;
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100.0%; Pred. No. 1.7; ive 0; Mismatches
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EMBL; AF314507; AAG40291.1; -
EMBL; AF314506; AAG40298.1; -
EMBL; AF314506; AAG40290.1; -
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Pfam; PF02382; RTX; 1.
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J. Bacteriol. 183:1394-1404(2001)
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Les 10; Conservative
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283 LAQRVAAGLS 292
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Pasteurellaceae; Mannheimia.
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                                 NCBI_TaxID=75985;
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Davies R.L., Whittam T.S., Selander R.K.;
Selander Diversity and Molecular Evolution of the Leukotoxin (lktA)
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314508; AAG40292.1;
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003343; Hemlysn_Ca_bind.
InterPro; IPR00355; RtxA.
Pfem; PF00353; Hemlysn_Ca_bind.
Pfem; PF00353; Hemlysn_Ca_bind.
Pfem; PF00353; Hemlysn_Cabind; 5.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.7;
iive 0; Mismatches 0; Indels
                                                                                                                    Pfam; PF00333, hamolysinCabind; 5.
Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNDWGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; RNOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102150 MW; D99C36DAS95B1624 CRC64;
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102132 WW; 4138ABSFAE2843B3 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                       Interpro; IPR001753; EncoA hydrtse.
Interpro; IPR001343; Hemlysn_ca_bind.
Interpro; IPR003995; RtxA.
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   EMBL; AF314522; AAG40306.1; -
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STRAIN=PH56;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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EMBL; AF314505; AAG40289.1; -.

InterPro; IPR001733; EnCoA_hydrtse.

InterPro; IPR001343; Hemlyen_ca_bind.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RTX; I.

IPRINTS; PR00481; RTX; I.

IPRINTS; PR00481; RTXTOXINA.

PRINTS; PR00466; ENCYL COA HYDRATASE; I.

SEQUENCE 953 AA; 102010 MW; DE48B28EEBEB9PB CRC64;
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EMBL; AF314509; AAG40293.1; -.

InterPro; IPR001733; EnCoA.hydrtse.

InterPro; IPR001343; Hemlysn.Ca_bind.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

InterPro; IPR003995; RtxA.

INTERPROSIDER INTY: 1.

IPRINTS; PR00146; RTXTOXINA.

IPROSITE; PS00166; ENOYL. COA. HYDRATASE; 1.

SEQUENCE 953 AA; 102078 WW; EF425243C8741EE4 CRC64;
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100.0%; Pred. No. 1.7;
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100.0%; Pred. No. 1.7;
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MEDLINE=21101823; Pubmed=11157953;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 100.
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nes 10; Conservative
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Gaps

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953 A.A.

Length 953; Indels

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InterPro; IPR01753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; Rt.A.
Pfam; PF00333; hemolysinCabind; 5.
Pfam; PF00333; hemolysinCabind; 5.
PRINTS; PR01313; CABNDWGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; P800166; ENCYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102218 MW; 04AB1715B819E571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF02382; RTX; 1.
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EMBL; AF414141; AAL13281.1;
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es 10; Conservative
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Pasteurella haemolytica.
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283 LAQRVAAGLS 292
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Matches
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STRAIN=PH292, and PH296;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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Bavies R.L., Campbell S., Whittam T.S.;

"Mosaic structure and molecular evolution of the leukotoxin operon
(lktCABD) of Mannheimia (pasteurella) haemolytica, Mannheimia
glucosida and Pasteurella trehalosi.";
J. Bacteriol. 0:0012090.

EMBL; AR314515; AAG40299.1;
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Pasteurellaceae; Mannheimia.
NCBL_TaxID=75985;
                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PRO0166; ENOYL, COA_HYDRATASE; 1.
SEQUENCE 953 Aa; 102043 MW; 488F11490479A69A CRC64;
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Last sequence update)
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Last annotation update)
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J. Bacteriol. 183:1394-1404(2001).
J. Bacteriol. 183:1394-1404(2001).
J. Bacteriol. 183:1394-1404(2001).
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PP00382; RTXA.
Pfam; PP00382; RTX, 1.
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                                                 PRT;
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J. Bacteriol. 183:1394-1404(2001).
                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2003 (TrEMBLrel. 23,
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                                               PRELIMINARY;
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                                                                    09EV30
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  RESULT 31
Q9EV30
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Mannheimia glucosida.
Bacteria; Proteobacteria, Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 Aa; 102236 Mw; AC5874B3B75D1C98 CRC64;
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Last annotation update)
                                                                                                                                                                          Davies R.L., Whittam T.S., Selander R.K.; "Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannheimia
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100.0%; Pred. No. 1.7;
ative 0; Mismatches
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                                                                                                                                                                                                                                    haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL: AF314519; AAG40303.1; -.
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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                                                                                                                                  STRAIN=PH240;
MEDLINE=21101823; Pubmed=11157953;
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265 LAQRVAAGLS 274
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                                                                                                               Pasteurella trehalosi.
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                                                                                                                                               NCBI_TaxID=47735;
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                                                        01-MAR-2001
                                                                                          Leukotoxin.
                                Q9EV22
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            RESULT 36
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                                 SEQUENCE FROM N.A.
STRAIN=PH202, and PH494;
Davies R.L., Whittam T.S., Selander R.K.;
Sequence diversity and molecular evolution of the leukotoxin (lktA)
gene in bovine and ovine strains of Mannheimia (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=PH254, PH246, and PH252;

STRAIN=PH254, PH246, and PH252;

Davies R.L., Whittam T.S., Selander R.K.;

"Sequence diversity and molecular evolution of the leukotoxin (lktA) agene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica.";

J. Bacteriol, 0.0-0(2001).

J. Bacteriol, 0.0-0(2001).

EMBL; AF314525; AAG40309.1;

EMBL; AF314523; AAG40309.1;

EMBL; AF314524; AAG40308.1;
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Pasteurellaceae; Pasteurella.
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL. COB HYDRATASE; 1.
SEQUENCE 954 AA: 102410 WW; 02A60E52411711A2 CRC64;
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955 AA; 102127 WW; 074B2E4ADFFF57AA CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       955 AA
                                                                                       haemolytica..;
J. Bacteriol. 0:0-0(2001).
EMBL, AR314513; AAG40297.1; -.
EMBL, AP314511; AAG40295.1; -.
InterPro; IPR001753; EnCoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemclysinCabind; 5.
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Pfam; PF02382; RTX; 1.
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PRINTS; PR01488; RTXTOXINA.
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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Best Local Similarity 100.
Matches 10; Conservative
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285 LAQRVAAGLS 294
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Q9EUD4
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MEDLINE-96065700; PubMed-7476166;
Ertesvag H., Hoidal H.K., Hals I.K., Rian A., Doseth B., Valla S.;
Ertesvag H., Hoidula H.K., Hals I.K., Rian A., Doseth B., Valla S.;
Extesvag H., Hoidular type mannurconan C-5-epimerase genes controls
alginate structure in Azotobacter vinelandii.";
Mol. Microbiol. 16:119-731(1995).
EMBL; L39096; AAA87311.1; -.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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100.0%; Pred. No. 1.7;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00313; hemolygincabind; 5.
Pfam; PF00313; hemolygincabind; 5.
PRINTS; PR01313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PR00166; BOYL COA HYDRATASE; 1.
SEQUENCE 955 AA; 102069 WW; PDCF2E99BBDC394F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Mannuroan C-5-epimerase.
                                                          16, Created)
16, Last sequence update)
23, Last annotation update)
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955 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haemolytica.";
J. Bacteriol. 183:1394-1404(2001).
EMBL; AF314526; AAG40310.1; -.
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn.Ca_bind.
InterPro; IPR003995; RtxA.
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Best Local Similarity 100.
Matches 10; Conservative
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PRELIMINARY;
                                                                                               01-MAR-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
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Q8YKJ3
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RX MEDLINE-20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballow R.M., Basud A., Baxendall J., Bayraktarolgu L., Bassley E.M.,

RA Ballow R.W., Baud A., Baxendall J., Bayraktarolgu L., Bassley E.M.,

RA Beeson K.Y., Banos P.V., Burman B.P., Bhandari D., Blolshakov S.,

RA Burtis R.C., Bucam D.A., Buller H., Cadieu E., Center A., Chadra I.,

RA Cherry J.M., Evangeliste C.C., Ferraz C., Ferriac C., Dearl, E., Dowles P., Davies P.,

RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Mayus P., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Moy M., Murphy S., Mosh M.-H., Ibeyam C.,

A Jalali M., Aslubh F., Karpen G.H., Kez J., Kenlow D.,

RA Harris N.L., Moy W., Murphy B., Mosh W. D., Yang S.,

RA Liu X., Matteri B., Modira C.D., Kraft C., Mcraid J., Mosh W. J.,

RA Bazzolo M. Pittman G.S., Pan S., Pollard J., Walson R.,

RA Shrakkas R., Tector C., Turner R., Venter E., Wang X.,

RA Shrakkas R., Tector C., Turner R., Venter E., Wang X.,

RA Wallam S.M., Woodage T., Singbeton M., Strong S., Zhu X., Smith H.O.,

RA Wallams S.M., Woodage T., Singbeton M., Strong S., Zhu X., Smith H.O.,

RA Wallams S.M., Woodage T., Worley C.M., Weissenbach J.,

RA Wallams S.M., Woodage T., Worley C.M., Weissenbach J.,

RA Wallams S.M., Woodage T., Singbeton R., Strong S., Zhu X., Smith H.O.,

RA The genome sequence
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                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                               1.1%; Score 10; DB 2; Length 1403;
100.0%; Pred. No. 2.5;
ive 0; Mismatches 0; Indels
                                       Pfam; PF00353; hemolyginCabind; 12.
SMART; SM00722; CASH; 4.
SMART; SM00710; PbH1; 15.
SEQUENCE 1403 AA; 147168 WW; 4E843AB0A366A95C CRC64;
                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
InterPro; IPR006633; CASH.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR006626; PbH1.
                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                              Query Match
Best Local Similarity 100.
Matches 10; Conservative
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1257 GDDLLDGGAG 1266
                                                                                                                                                                                                                                                                             PRELIMINARY;
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CG5833 OR CG13132.
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Q9VL42
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SEQUENCE FROM N.A.

Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Celniker S.E., Adams M.D., Ananatides P.G., Brandon R.C., Rogers Y.,

Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,

Carlson J., An H., Baldwin D., Barzon J. Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Carlson J.W., Houck J., Hoskins R.A., Hostin D., Howland R.A.,

Dodson T.C., Moy M., Wurphy B., Nelson K.A., Nelson K.A., Nunco J.,

Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Rapilams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnniker S.E., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Kubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AB003627; AAF52856.2;
FlyBase; Fegn003190; CG5833.

InterPro; IPR001879; horm_receptor.

InterPro; IPR001879; horm_receptor.

InterPro; IPR00110; Ig-like.

PERSTE; SM00409; IG; 1.

PROSITE; PS50227; G PROTEIN RECEP_F2_3; 1.

PROSITE; PS50835; IG_LIKE; 1.

SEQUENCE 1424 AA; I52768 MW; E8E39E276FD7414E CRC64;
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., SaBamoto S.,
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NCBL_TaxID=103690;
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Last annotation update)
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100.0%; Pred. No. 2.5;
ative 0; Mismatches
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
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Plasmid pCC7120alpha.
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Best Local Similarity
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MEDINE=970031; PubMed=8843436;
REGENDES M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered coosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing
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                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00166; Calx-beta; 5.

Pfam; PF00166; Calx-beta; 5.

Pfam; PF001623; hemolysincabind; 25.

Pfam; PF00182; peptidase_S8; 1.

R PRINTS; PR00723; SUBTILISIN.

R SWART; SW00736; CABCG; 2.

R SWART; SW00736; CALX-beta; 6.

R PROSITE; PS00136; EF_HAND; 1.

R PROSITE; PS00136; SUBTILASE, 6.

R PROSITE; PS00136; SUBTILASE, 8.

R PROSITE; PS0136; SUBTILASE, 8.

R PLASMIG; Hypothetical protein; Complete protecome.

SEQUENCE 4936 AA; 519407 MW; FB5A8323CB29C828 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SCO2043.
SCO2043 OR SCE20.17C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                           cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003600; BAB78388.1; -.
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100.0%; Pred. No. 8;
tive 0; Mismatches
                                                                                                                                                                                                                                             Interpro; IPR006644; Cadg.
Interpro; IPR003644; Calx_beta.
Interpro; IPR002048; EF-had.
Interpro; IPR001343; Henlysn.Ca bind.
Interpro; IPR000209; Peptidase_58.
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Best Local Similarity 100.
Matches 10; Conservative
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098DA8
AC 098DA
AC 098DA
DT 01-MA
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Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandrem M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Squares R., Squares R., Squares C., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 41:141-147(2002).
EMBL; AL939114; CA565573.1;
InterPro; IPR005837; Hydrolase.
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TIGRRAMs, TIGR01460, HAD-SF-11A, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 259 AA, 28059 WW, 997D2581D4F7835A CRC64;
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100.0%; Pred. No. 5.5;
rative 0; Mismatches
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Job time : 85 secs
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6: /cgn2_6/ptodated1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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50.2%; Score 2334; DB 1; Length 1
Best Local Similarity 50.1%; Pred. No. 5.2e-174;
Matches 465; Conservative 175; Mismatches 263; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/777,715
FILING DATE: 19911016
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 29310-2001320
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-327-2951
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/0777715
; Sequence 7, Application US/0777715
; Patent No. 5273889
; GENERAL INFORMATION:
APPLICANT: Potter, Andrew
APPLICANT: Campos, Manuel
APPLICANT: Campos, Manuel
APPLICANT: Campos, Manuel
APPLICANT: Hughes, Huw P.A.
TITLE OF INVENTION: CYTOKINE-LEUKOTOXIN GEN
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
COURTE: Anidolefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
                                                                                    US-09-062-126-3
US-08-258-188-2
VCT-US95-08554-2
US-08-387-156-10
US-08-878-156-10
US-09-124-491-10
US-09-124-491-16
US-09-124-491-16
US-09-124-491-16
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 anino acids
TYPE: AMINO ACID
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CARACTES CONTRACT
CALLES E REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PROBLEM #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,126
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                               CLASSIFICATION: 5.5.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/777,715
PRIOR APPLICATION NUMBER: US 07/777,715
PRIOR APPLICATION NUMBER: US 07/571,301
ATTORNEY AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 30,000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
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                            289 GIQSILGSVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEPGEQISQ
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         AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS
                                                                             TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK
                                                                                                                                                LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA
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                                                       8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET
                                                                                                              AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS
                           Gaps
                           26;
 Length 1098;
                           Indels
Query Match 50.2%; Score 2334; DB 1; Best Local Similarity 50.1%; Pred. No. 5.2e-174; Matches 465; Conservative 175; Mismatches 263;
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Sequence 2, Application US/08170126
Patent No. 5594107
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW
APPLICANT: CAMPOS, MANUEL
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: CYTOKINE-CYTOTOXIN GENE FUSIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 6

US-08-170-126-2

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                                                                           GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
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                        ---AETEGTDEIGLIVNAKAGNDDIFVGQ 597
KHIKADKLVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLN 707
                                       US-08-954-418-2

Sequence 2, Application US/08954418

Sequence 2, Application US/08954418

Patent No. 6096320

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW
APPLICANT: CAMPOS, MANUEL
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
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COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,418
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/170,126
APPLICATION NUMBER: 08/7/1,301
APPLICATION NUMBER: 08/7/1,301
APPLICATION NUMBER: 08/7/1,301
APPLICATION NUMBER: 08/7/1,301
APPLICATION NUMBER: 33,208
REGISTRATION NUMBER: 9000-0013.21
TELEPHOCAPOCKET NUMBER: 9000-0013.21
TELEPHONINICATION INFORMATION:
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TELEPHONINICATION INFORMATION:
TELEPHONINICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
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                        FGRVKNWQVTDGEASSKLDFSKVIQRV----
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STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
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                                                                                                26;
                                                              Length 1098,
                                                                                                  Indels
                                                             Query Match 50.2%; Score 2334; DB 3; Best Local Similarity 50.1%; Pred. No. 5.2e-174; Matches 465; Conservative 175; Mismatches 263;
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              MOLECULE TYPE: protein
linear
                               US-08-954-418-2
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602 664 661 724 720 784 780

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APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: HAEMOPHILUS SOMNUS OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                       841 GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 VAGVTGLISGILEASKOAMFESVANRLOGKILEWEKONGGONYFDKGYDSRYAAYLANNL
                                                                              432 KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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APPLICATION NUMBER: US/07/908,253
FILING DATE: 19920702
CLASSIPICATION: 420
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-908-253-2
; Sequence 2. Application US/07908253
; Patent No. 5534256
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: DEM PC COMPATIBLE
COMPUTER: DEM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,812
FILING DATE: 15-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/038,719
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                            GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: THEISEN, MICHAEL
APPLICANT: HARLAND, RICHARD J.
APPLICANT: HARLAND, RICHARD J.
APPLICANT: HARLAND, RICHARD J.
APPLICANT: HARLAND, ACCINES FOR HAEMOPHILUS SOMNUS NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROSINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9000-0019.20
                                                                                                                                                                                                                        ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-6999
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                        Sequence 8, Application US/08619812
Patent No. 6100066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 924 amino acids TYPE: amino acid
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MOLECULE TYPE: protein
                       US-08-619-812-8
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                                                                                                                                   Gaps
                                                                                                                                   25;
                                                                                                           50.1%; Score 2326.5; DB 1; Length 926; 50.0%; Pred. No. 1.5e-173;
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                                                                                                         Query Match 50.1%; Score 2326.5; DB 1; Best Local Similarity 50.0%; Pred. No. 1.5e-173; Matches 461; Conservative 174; Mismatches 262;
TELEFAX: (415) 327-3231
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 926 amino acids TYPE: AMINO ACID TOPOLOGY: linear MOLECULE TYPE: protein
                                                                            ; MOLECULE TY
US-07-908-253-2
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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                                                                                                                                                                                         ENHANCED IMMUNOGENICITY USING LEUKOTOXIN CHIMBRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.1%; Score 2326.5; DB 1; Lengun
Best Local Similarity 50.0%; Pred. No. 1.5e-173;
Matches 461; Conservative 174; Mismatches 262; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION UNMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
TELECOMMINICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          3: REED & ROBINS
285 HAMILTON AVENUE, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA COUNTRY: UNITED STATES OF AMERICA
| ::| : | : | ETSSNDSRNVLVAPTSMLDQSL 917
                                                                                                                                ; Sequence 2, Application US/08455970A; Patent No. 5708155
                                                                                                                                                                                                       APPLICANT: POTTER, ANDREW A. APPLICANT: REDNOND, MARK J. APPLICANT: HUGHES, HUW P.A. TITLE OF INVENTION: ENHANCED I TITLE OF INVENTION: CHIMERAS CORRESPONDENCE ADDRESS: ADDRESSEE: REED & ROBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                       GENERAL INFORMATION:
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TYPE: amir
TOPOLOGY:
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               303 YAERFKKIGYDGDNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAGSVIASPIALL
                                                                       543 KITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKĒTKIJAKLGEĞDDNVFVGSĞTTEIDĞ
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FAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL
                                                       VAGVTGLISGILEASKOAMFESVANRLOGKILEWEKONGGONYFDKGYDSRYAAYLANNL
                                                                                                               KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
SPETATION SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHIMERAS
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Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HUGHES, HUW P.A.
TILLE OF INVENTION: GARH-LEUKOTOXIN CH:
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
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372 VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
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50.1%; Score 2326.5; DB 1; Length
Best Local Similarity 50.0%; Pred. No. 1.5e-173;
Matches 461; Conservative 174; Mismatches 262; Indels
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US 07/779,171
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acid
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242

311 302 371 362

251

491 482 542

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664 661 724

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VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
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                                                 252 VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
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                                                                                                                                                                                                                                                                                                                                                                         552 QVTDGEASSKLDFSKVIQRV----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/08878748
; Patent No. 5969126
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J. APPLICANT: HUGHES, HUW P.A. ITLLE OF INVENTION: GRH-LEUKK NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
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                                                                                                                                   GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA 895
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
POTTER, ANDREW A.
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUITE 200
                                                                                                                                                                              FGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                            FTSSNDSRNVLVAPTSMLDQSL 917
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NAME: MCCRACKEN, THOWAS P.
REGISTATION UNDBER: 36,548
REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                      E: REED & ROBINS LLP
285 HAMILTON AVENUE,
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INFORMATION FOR SEQ ID NO: 6:
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amino acid
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LENGTH: 926 amino acid
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Sequence 2, Application US/08535837

Patent No. 5985289

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
ITILE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
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                                                                                                                    IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
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MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTATION UNDMER: 33,208
REFERENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
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            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acida TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROBINS, ROBERTA L.
                                                                                                                            19-NUL-61
                                                 CURRENT APPLICATION DATA APPLICATION NUMBER: UK
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                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-878-748-6
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Version #1.30

YSTEM: PC-DOS/MS-DOS Patentin Release #1.0,

USA 94301

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NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,865
FILING DATE: 09-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY AGENT INFORMATION:
                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
           STATE: C. COUNTRY:
                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-124-491-6
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                                                                  492 NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW 551
                                                                                                                                                                                                                                                                                                                                                                                                                                     QVTDGEASSKLDFSKVIQRV----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KITDGAASSTFDLTNVVORIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 724
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VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
              TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                                                                                                      AKGFSNIGNKLONL-NPSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO 251
                                                                                                                                                          VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE 311
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FTSSNDSRNVLVAPTSMLDQSL 917
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US-09-124-491-6
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: 926 amino acids amino acid TYPE: protein

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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                15 INSTKSGLKNLYLAIPKD--YDPOKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                 25;
   Length
 DB 3;
50.1%; Score 2326.5; DB 3;
llarity 50.0%; Pred. No. 1.5e-173;
Conservative 174; Mismatches 262;
                Similarity
                               461;
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 Query Match
Best Local
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CHIMERAS

Sequence 6, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GARH-LEUKCTOXIN CHIMERA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROSHINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200

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; TYPE: ami
; TOPOLOGY:
; MOLECULE TYE
US-09-383-912-6
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                             784
KFLLNLNKELQAERVIAITQQQWDNNIGDLAGISRLGEKVLSGKAYVDAFEEGKHIKADK 482
                                           NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW 551
                                                                                                                                                                                                                                            LVQLDSANGIIDVSNSGKAKTQHILFRTPLLTPGTEHRERVQTGKYEYITKLNINRVDSW
                                                                                                                               QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                                                                                   GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
                                                                                                                                                                                                                                                                                                       IQYRDYBLRKVGYGYGYGTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
                                                                                                                                                                                                                                                                                                                                                                                             DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLONYQSNKTDHKIEQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN TOWNER TOWNER TOWNER TOWNEY TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER TOWNER
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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REGISTRATION NUMBER: 38,548
REPERENCE/DOCKET NUMBER: 900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
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TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
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                                                                                                                                                                                                                                                                                                                     Length 926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 461; Conservative 174; Mismatches 262;
                                                                                                                                                                                                                                                                                                                     50.1%; Score 2326.5; DB 50.0%; Pred. No. 1.5e-173
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FTSSNDSRNVLVAPTSMLDQSL 917
                                                                                                              MOLECULE TYPE: protein
amino acid
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GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POTTER, ANDREM A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: ENHANCED IMMUNOGENICITY USING LEUKOTOXIN
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: 31-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.1%; Score 2326.5; DB 1; Best Local Similarity 50.0%; Pred. No. 1.6e-173; Matches 461; Conservative 174; Mismatches 262; I
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REPERBUNCF/OCKET NUMBER: 9001-0016.10
TELECOMOUNICATION INFORMATION:
TELEPAN: (415) 327-3400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNITED STATES OF AMERICA
                                                                                                                                                                                                          FTSSNDSRNVLVAPTSMLDOSL 917
                                                                                                                                                                                       FGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                    ; Sequence 12, Application US/08455970A; Patent No. 5708155; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   936 amino acids
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                                                                APPLICANT: POTTER, ANDREW A.

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN; COMPOSITIONS AND USES THEREOF; NUMBER OF SEQUENCES: 8

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/15,537

FILING DATE: 09-FEB-1993

APPLICATION NUMBER: 504,850

FILING DATE: 05-APR-1990

APPLICATION NUMBER: 335,018

FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                     Query Match 50.1%; Score 2326.5; DB 6; Length Best Local Similarity 50.0%; Pred. No. 1.5e-173; Matches 461; Conservative 174; Mismatches 262; Indels
                                                       5476657
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50.1%; Score 2326.5; DB 1; Length
Best Local Similarity 50.0%; Pred. No. 1.6e-173;
Matches 461; Conservative 174; Mismatches 262; Indels
                                   COMPUTER: REALIZE FORDY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,970A
FILING DATE: J1-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION HATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 10:
SEQUENCE CRARACTERISTICS:
LEMOTH: 943 amino acids
AMERICA
UNITED STATES OF
                                                                                                                                                                                                                                                                                                                                          : 943 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                           COMPUTER READABLE FORM
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US-08-455-970A-10
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TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                  VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE 311
                                                                                                                                                                                                                                                                                                 KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS 491
                                                                                                                                                                                                                                                                                                                                                           NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW 551
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| Patent No. 5708155
| GENERAL INFORMATION:
| APPLICANT: POTTER, ANDREW A. APPLICANT: HUGHES, HUW P.A.
| APPLICANT: HUGHES, HUW P.A.
| TITLE OF INVENTION: CHIMERAS | TITLE OF INVENTION: CHIMERAS | TITLE OF INVENTION: CHIMERAS | TITLE OF INVENTION: APPLICANT: ADDRESSE: REED & ROBINS | SUTRE 200 | STREET: 285 AMMILTON AVENUE, SUITE 200 | CITY: PALO ALTO | STREET: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGTANSVSSNALQPITQPTQGI 922
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US-08-455-970A-10
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243 VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES 302
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            LINSTKSGLKNLYLAIPKD - YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                             73 VNOFLSLTQTGIAISATKLEKFLOKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
                                                                                                                                                                                       193 AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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APPLICANT: POTTER, ANDREW A. APPLICANT: REDMOND, MARK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-387-156-8
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               IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
                                                                                                                 DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY I FRKGDGNDTLYDGTGNDKLA
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Sequence 14, Application US/08455970A

Patent No. 5708155

GENERAL INFORMATION

APPLICANT: REDMOND, MARK J.

APPLICANT: HUGHES, HUW P.A.

TITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS: 15

CORRESPONDENCE ADDRESS: 15

CORRESPONDENCE ADDRESS: 15

CORRESPONDENCE ADDRESS: 15

CORRESPONDENCE ADDRESS: 15

CORRESPONDENCE ADDRESS: 15

COURTY: ADLO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
FILING DATE: 31-MAY-1995
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSITIANIUS: 14-3
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-607-1992
ATYORNEY AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REPERENCE/DOCKET NUMBER: 9001-0016.1
TELEPHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                              FGTANSVSSNALQPITQPTQGI 922
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                      DRIFGGKGNDRISGDEGDDLIDGGSGDDVINGGAGNDVYIFRKGDGNDTLYDGTGNDKLA 784
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                                                                                                                                        QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPAGED COMPAGED COMPUTER: DESTRUING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/694,865 FILING DATE: 09-AUG-1996
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Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRRH-LEUKOTOXIN CHI;
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::| : | :
FTSSNDSRNVLVAPTSMLDQSL 917
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAWE: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REPRENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 977 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STREET: 285 HAMI
CITY: PALO ALTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
                            GRRH-LEUKOTOXIN CHIMERAS
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
                                                                                  STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 327-3231
INFORMATION FOR SEQ 1D NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TYPE: amino acid
          APPLICANT: HUGHES, HUW P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein US-08-387-156-8
                            TITLE OF INVENTION: Gn
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                           15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                  25;
                                       Length 977;
                                                                  Indels
                                        DB 2;
                                    Query Match 50.1%; Score 2326.5; DB 2; Best Local Similarity 50.0%; Pred. No. 1.7e-173; Matches 461; Conservative 174; Mismatches 262;
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; MOLECULE TYPE: protein US-08-694-865-8
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RESULT

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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: EM PC Compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIFICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
RIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
RIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 16-OCT-1991
APPLICATION NUMBER: US 07/79,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.1%; Score 2326.5; DB 2; Best Local Similarity 50.0%; Pred. No. 1.7e-173; Matches 461; Conservative 174; Mismatches 262;
                                                                     APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
8, Application US/08878748
3, 5969126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      S: REED & ROBINS
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TOPOLOGY: linear
                                                   GENERAL INFORMATION:
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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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         PFILING DATA: 10.75.

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/960,932

PFILING DATE: 14-0CT-1992

PFILING DATE: 14-0CT-1992

PRIOR APPLICATION DATA: DOTA-1991

APPLICATION NUMBER: US 07/79,171

FFILING DATE: 16-0CT-1991

ATTORNEY/AGENT INFORMATION: NAME: MCCRACKEN, THOMAS P. REGISTRATION NUMBER: 38,548

REFERENCY/DOCKET NUMBER: 9001-0016.22

TELECOMMUNICATION INFORMATION: TELEPHONE: (415)327-3340

TELEPHONE: (415)327-3340

TELEPHONE: (415)327-3360

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               977 amino acids
                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-124-491-8
                                                                                                                                                                                                                                                             amino acid
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                                             VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
                                                                                                                                                                   NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: A PC-DOS/MS-DOS
SOSTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: POTTER, ANDREW A.

APPLICANT: MANNS, JOHN G.

TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
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Patent No. 6022960
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US (
FILING DATE: 09-AUG-199
APPLICATION NUMBER: US (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSOSTQTIEAFSSQLAKLGSTISQ 192
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                                                                                                   193 AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO
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Patent No. 5273889
GENERAL INFORMATION:
POLICANT: POLICE, Andrew
APPLICANT: Potter, Andrew
APPLICANT: Hughes, Huw P.A.
ITILE OF INVENTION: CYTOKINE-LEUKOTOXIN GENE
ITILE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE S.
STREET: S45 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGTANSVSSNALQPITQPTQGI 922
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                                                                                                                                                                                                                              GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09383912
Patent No. 6521746
GENERAL INFORMATION
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TILLE OF INVENTION: GMRH-LEUKOTOXIN CHI
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE
                                                                                                                                                                                                                                                                                                                                  FGTANSVSSNALQPITQPTQGI 922
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-383-912-8
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STATE: CA
COUNTRY: USA
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                                        665 IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 724
                                                                                                                   725 DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA 784
GEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEK 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0013.21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,126
FILING DATE: 20-DEC-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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FTSSNDSRNVLVAPTSMLDQSL 917
                                                                                                                                                                                                                                                                                                                                                        FGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/08170126; Patent No. 5594107; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069 amino acids
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APPLICATION NUMBER: U
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94301
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                                                                                                               CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/77,715

FILING DATE: 19911016

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: RODINS, RODERTA I.

REGISTRATION NUMBER: 33,208

REGISTRATION NUMBER: 29310-2001320

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: 415-327-7250

TELEPAX: 415-327-2951
                                      COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 1069 amino acids
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12;

Gaps

25;

Indels

Length 1069;

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CYTOKINE-CYTOTOXIN GENE FUSIONS AND THEREOF
                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0013.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
INFORMATION FOR SEC ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/954,418
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/170,126
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/571,301
ATTORNEY/AGENT INFORMATION:
                                                                                          STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MC-
                                                    3: REED & ROBINS
635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                            1069 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
 TITLE OF INVENTION: CY
TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                    ADDRESSEE: REED GETREET: 635 BRYALCITY: PALO ALTOSTATE: CALIFORNI
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                                                    VNOFLSLTQTGIAISATKLEKFLOKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                                                                                        TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
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                   QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
  LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
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FTSSNDSRNVLVAPTSMLDOSL 917
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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                         15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
  DB 3; Length 1069;
Query Match 50.1%; Score 2326.5; DB 3
Best Local Similarity 50.0%; Pred. No. 1.9e-173;
Matches 461; Conservative 174; Mismatches 262;
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Sequence 4, Application US/08954118 Patent No. 6096320 GENERAL INFORMATION: APPLICANT: POTTER, ANDREW

US-08-954-418-4

CAMPOS, I

APPLICANT: APPLICANT:

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STRAIN: 5943
IMMEDIATE SOURCE:
SOURCE
                                                             US-08-215-805A-80
          ORGANISM:
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                                                                                                                                                                                                                                                GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                                     604
                                                                                                GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET 664
                                                                                                                                          IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 724
                                                                                                                                                                                      DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA 784
          NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW 551
                                                      QVTDGEASSKLDFSKVIQRV----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
TITLE OF INVENTION: SUIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19603/61 (D-1329A)
                                                                                                                                                                                                                                                                                                                          FGTANSVSSNALQPITQPTQGI 922
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; Sequence 80, Application US/08215805A
; Patent No. 5559008
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 1960:
TELECOMMUNICATION INFORMATION:
TELEFAX: (716) 263-1636
TELEFAX: (716) 263-1636
INFORMATION FOR SEQ ID NO: 80:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 934 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLLGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKONGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQORWDNNIGELAGIT 465
                                                                                                                                                                                                                                                                                                                           47 AADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKG 106
                                                                                                                                                                                                                                                                                                                                                                                                                     107 LDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEII 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITS 285
                                                                                                                                                                                                                                                                  RKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 KLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAG
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                                                                                                                                                  DB 1; Length 934;
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                                                                                                                                             Query Match 49.4%; Score 2297.5; DB 1; Length: Best Local Similarity 49.7%; Pred. No. 2.9e-171; Matches 469; Conservative 172; Mismatches 254; Indels
                                                         LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CLONE: (Lambda)yfc33-37
Pasteurella suis
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us-10-069-799-5.rai

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NNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNCKKTQAL 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  746 DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVK 805
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                                                                                      TIEASLITISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVA 395
                                                                                                                                                            396 NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD 455
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; Sequence 8, Application US/09062126
; Patent No. 6500435
; GENERAL INFORMATION:
; APPLICANT: Kamp, Elbarte Margriet
; APPLICANT: Smits, Marinus Adrianus
; ITILE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; FILE REFERENCE: 470-980537
; CURRENT APPLICATION NUMBER: US/09/062,126
; CURRENT APPLICATION NUMBER: US/09/062,126
; PRIOR FILING DATE: 1995-06-09
; PRIOR FILING DATE: 1993-10-15
; PRIOR APPLICATION NUMBER: 07/722,971
; RING APPLICATION NUMBER: 07/722,971
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FaetSEQ for Windows Version 3.0
; TENCOR DO 08
                                       516 HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ::| ||::||: | ||::||: || ||:||| || AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST 275
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                                                                                            53;
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48.1%; Score 2236.5; DB 3; Length 956;
Best Local Similarity 47.7%; Pred. No. 1.8e-166;
Matches 453; Conservative 188; Mismatches 255; Indels 53;
                  925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION STSIEM:
SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,270A
FILING DATE: December 23, 1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Michaline
REGISTRATION NUMBER: 40,261
REGISTRATION NUMBER: 40,261
RELEPHONE: (416) 364-7311
TELEFORMINICATION INFORMATION:
TELEFAK: (416) 361-1398
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Actinobacillus pleuropneumoniae
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893 E--SSALLKESKFASNSLNKLVSSAAHL-
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 956 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Canada
ZIP: M5H 3Y2
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                                                             KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNOFLSLTOTGIAISATKLEKFLQ
                                                                                                                                    ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL
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Best Local Similarity
Matches 453; Conserv
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Sequence 10, Application US/09062126 Patent No. 6500435 GENERAL INFORMATION:

RESULT 28 US-09-062-126-10

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KRQAKKGYDVTKNGLQYGVSQAKLQALGAGKAVQKYGNKLVLVIPKEYDGSVGNGFFDLV
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APPLICANT: Smits, Marines Adrianus
TITLE OF INVENTION: Recombinant Vaccine For Prevention
TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
FILE REFERENCE: 470-980537
CURRENT APPLICATION NUMBER: US/09/062,126
CURRENT APPLICATION NUMBER: US/09/062,126
FRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 08/488,706
PRIOR FILING DATE: 1995-06-09
PRIOR FILING DATE: 1993-10-15
PRIOR FILING DATE: 1993-10-15
PRIOR FILING DATE: 1991-06-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NOS: 15
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Best Local Similarity 42.1%; Pred. No. 4.7e-142;
Matches 420; Conservative 168; Mismatches 290;
                                                                                                                                                                                                                                                                                               ; ORGANISM: Actinobacillus pleuropneumonia
US-09-062-126-10
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                                   KAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAK 105
                                                                                                                     GITKLGERIKSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFT
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                                                               79 KAARELGIQVKYVNRNELEVAHKSLGTADQPLGLTERGLTLFAPQLDQFLQKHSKISNVV
                                                                                                106 GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                                                                                                                                                   166 IGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN---FSKTNLGLEIITGLL
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GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: Recombinant Vaccine For Procine
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                                                                                                                                                                                                                       SHNNGVLTIKDWF-----KEGNKYNHKIEQIVDKNGRKLTAENLGTYFKNAPKADNLL 964
                      792 EGNDKLLGGGNGNNYLSGGDGNDELQVLGKWFLMCFVAVKAMINFMVAQVLIYLDGGEGND 851
                                                                    --LLDGGSGDD
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   EEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDD----
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AS VACCINES
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43.0%; Pred. No. 6.7e-142;
tive 152; Mismatches 296; Indels 120
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AND THEIR USE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL
TITLE OF INVENTION: PRODUCING SAME,
UNDBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/08772270A
Patent No. 6019984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTOWNEY, ASSETS

NAME: Gravelle, Micheline
REGISTRATION NUMBER: 65.
REFERENCE/DOCKET NUMBER: 65.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bereskin & Parr
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INPOWATION FOR SEG ID NO: 1.
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: MacInnes, Janet
APPLICANT: Ricciatti, Paul
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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Best Local Similarity
Matches 428; Conserva
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STRANDEDNESS: Bil
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     964 EGDDKLLGGONGNNYLSGGDGNDELQVLGNGFNVLRGGKGDDKLYGSSGSDLLDGGEGNDY 1023
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                                                                            462
                                                                                                571 VAETEGIDEIGLIVNAKAGNDDIFVGQGKWNIDGGDGHDRVFYSKDGGFGNITVDGTSAT 630
                                                                                                                                                                                                                                                                                                                                                                                                                              904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754 INGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVK--RND 808
                                                                                                                                                                                                                                                                                                                                   631 EAGSYTVNRKVARG-DIYHEVVKRQETKVGKRTETIQYRDYELRKVG-YGYQSTDNLKSV 688
                                                                                                                                                                                                                                                                                                                                                                                                             GITKLGERIKSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFT
TISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
                        550 TISTALSAIAAGTAAASAGALVGAPITLLVTGITGLISGILEFSKQPMLDHVASKIGNKI
                                                                                                                                                                                                                                  SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDG--EASSKLDFSKVIQR-----
                                                                            LEWEKONGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQORWDNNIGELA
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; Sequence 2, Application US/08772270A
; Sequence 2, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
    APPLICANT: MacInnes, Janet
    APPLICANT: MacInnes, Janet
    APPLICANT: Ricciatti, Paul
    APPLICANT: Rosendal, Sonnie
    TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
    ITILE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
    NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Bereskin & Parr
    STREET: 40 King Street West
    CITY: Toronto
    STREET: Ontario
    COUNTRY: Canaa---
ZIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    689 EEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,270A
FILING DATE: December 23, 1996
CLASSIFICATION: 424
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 41.4%; Score 1924; DB 5; Length 1244; Best Local Similarity 43.0%; Pred. No. 8.7e-142; Matches 428; Conservative 152; Mismatches 296; Indels 120;
                                                                                                                                                   ZIP: 14202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PREST FLOPPY MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinobacillus pleuropneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19603/00001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: Serotypes 2, 3, 4, 6 and 8 INDIVIDUAL ISOLATE: Swine CELL TYPE: Gram negative bacterium
      IIILE OF INVENTION: Pleuropneumoniae
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/972,229
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,932
REGISTRATION NUMBER: 33,932
REFERENCE/DOCKET NUMBER: 19603
TELEPONE: 716-853-8109
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1244 amino acids
                                                          ADDRESSEE: Alan S. Korman STREET: 1600 Empire Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: double
TOPDLOGY: linear
MOLECULE TYPE: peptide
                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                          CITY: Buffalo
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-10500-2
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81 NGTALAKELFGTTEKLLGFSERGIALFAPQFDKLLNKN--QKLSKSLGGSSEALGQRLNK 138
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                                                                                                                                                           ---KLAFADANI----SDIMIERTKEGIIVKRNDHSG-SINIPR
                                                                                               WYITSNLONYOSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADEN
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kamp, Elbarte Margriet
APPLICANT: Smits, Marinus Adrianus
TITLE OF INVENTION: Recombinant Vaccine For Prevention
TITLE OF INVENTION: Recombinant Vaccine For Prevention
TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
FILE REPERENCE: 470-980537
CURRENT APPLICATION NUMBER: US/09/062,126
CURRENT FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 08/138,609
PRIOR FILING DATE: 1993-10-18
PRIOR PILING DATE: 1993-10-18
PRIOR APPLICATION NUMBER: 07/722,971
PRIOR PILING DATE: 1991-06-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE FEASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 KSNIQAGLNSTKSGL-----KNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
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Best Local Similarity 40.1%; Pred. No. 2.1e-128;
Matches 401; Conservative 180; Mismatches 308; Indels 111;
                                                                                                                                                                                                                            YN---ALPQLRKDIEQIISSTGAFTGDHGKVSVGSGGPL 1001
                                                                                                                                                                                                        878 KSQKLSASDIASSLNKLVGSMALF-GTANSVSSNALQPI 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Actinobacillus pleuropneumonia
US-09-062-126-3
                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/09062126; Patent No. 6500435
                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASTGKKVAAGFELSNQVIGNVTKAISSYVLAORVAAGLSTTGAVAALITSSIMLAISPL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 AFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNY 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 IYHEVVKRQETKVGKRTETIQYRDYELR--KVGYGYQSTDNLKSVEEVIGSQFNDVFKGS 703
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                                                                                                                                                                                                                                                                                     37.9%; Score 1763.5; DB 3; Length 1022;
.larity 40.0%; Pred. No. 2.4e-129;
Conservative 181; Mismatches 309; Indels 109;
                                                                                                                                                                                                    MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
           NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REESPERNCE/DOCKET NUMBER: 6580-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 400; Conservat
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                                                                                                                                                            amino acid
                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: cir
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                                                                                                                                                                                                                                  Length 758;
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29.6%; Score 1376.5; DB 1;
Best Local Similarity 40.5%; Pred. No. 3.2e-99;
Matches 304; Conservative 129; Mismatches 225; 1
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280206, DHHSE135940
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 543-5600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 DENKSOKLSASDIASSLNKLVGSMALFGTAN 905
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LENGTH: 758 amino acids
TYPE: amino acid
                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-258-188-2
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US-08-526-813-2
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APPLICANT: HALL,
APPLICANT: XU, Jian Guo
TITLE OF INVENTION: AN NEW AND DISTINCTIVE DNA SEQUENCE OF E.
TITLE OF INVENTION: coli 0157:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                       850
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                                                                                                                    KAYADAFEDGKKVEAGSNITLDAKT----GIIDISNSNGKKTQALHFTSPLLTAGTESR
                                                                                                                                                                                                                                                    G--NDDIFVGOGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-ARG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,188
FILING DATE: 14-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08258188 Patent No. 5475098
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
TUPE: READAPLE
TUPE: TRANS.
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APPLICANT: HALL, Robert H.

APPLICANT: HALL, Robert H.

APPLICANT: TY, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.

TITLE OF INVENTION: SPECIFIC DETECTION OF 0157:H7 AND OTHER ENTEROHEMORRHAGIC
TITLE OF INVENTION: E. coli
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                          742
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583 IVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVA 642
                                                                                                             ----EGDDLLDGGAGDDRLFGGKGNDRLSGDEGD
                                                                                    643 RGD--IYHEVVKRQETKVGKRIETIQYRDYELRKVGYGYGYGSTDNLKSVEEVIGSQFNDVF
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Pred. No. 3.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08554
FILING DATE: 14-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15280206, DHHSE135940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKEY NUMBER: 15280206
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                               APPLICANT: Hall, Robert H.
APPLICANT: Xu, Jian Guo
TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.
Patent No. 5756293
TITLE OF INVENTION: Specific Detection of 0157:H7 and Other Enterohemorrhagic TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 NGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLG 468
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                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,813
FILING DATE: 11-SEP-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                       Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 15280-206-1
TELECOMMUNICATION INFORMATION:
TELEPRA: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,188
FILING DATE: 14-UN-1994
ATTORNEY/AGENT INFORMATION:
      2, Application US/08526813
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amino acid
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                                                                                                                                                                                                                                                                                                              San Francisco
California
                           Patent No. 5756293
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            94111-3834
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                         FALADKNASTGKKVAAGFELSNOVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIM 288
                                                                          LAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTAL 348
                                                                                         GAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQ 408
                                                                                                                                             NGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLG 468
                                                                                                                                                                                             IVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVA 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERIKSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTA 524
                                                                                                                                                                                                                                                                                  GTESRERLINGKYSYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGL 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                       KGSKFNDI FHSG------EGDDLLDGGAGDDRLFGGKGNDRLSGDEGD
304; Conservative 129; Mismatches 225; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DENKSQKLSASDIASSLNKLVGSMALFGTAN 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITED STATES OF AMERICA
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Patent No. 5723129
GENERAL INFORMATION:
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635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 625 BRYANT ST
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATE
ZIP: 94301
COMPUTER READABLE FORM:
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492 NITLDAKTGIID-----ISNSNGKKTQALHFTSPLLTAGTESRERL---TNGKYS 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO
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                                                           Version #1.25
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                                                                                                                                     FILING DATE: 10-FEB-1995
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/779,171
ATPOREY/AGENT INFORMATION:
ATRIESTATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 617-8999
TELEFRAX: (415) 617-8999
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSLQFARGSQHWSYGLRPGSGSQDWS 510
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, TURRENT APPLICATION DATA: 105/08/387,156 FILING DATE: 10-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.5%;
Best Local Similarity 38.7%;
Matches 220; Conservative
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amino acid
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432 KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS 491
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SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/8748
FILING DATE: 19-JUN-1997
CLASSIFICATION 1536
PRIOR APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
APPLICATION NUMBER: US 07/960,932
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAMME: ROBINS, ROBERTA L.
NAMME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08878748
Patent No. 5569126
GENERAL INFORMATION:
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
ITILE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSE:
STREET: 635 BRYANT STREET
                                                                                                                                                                            539 YINKLKFGR-VKNWQVTDGEASSKLDFS 565
                                                                                                                                                                                                          483 SLSSLQFARGSQHWSYGLRPGSGSQDWS 510
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STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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US-08-878-748-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
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19.5%; Score 904.5; DB 2; Length 544;
Best Local Similarity 38.7%; Pred. No. 1.9e-62;
Matches 220; Conservative 98; Mismatches 169; Indels 81
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
                                                               Sequence 10, Application US/08694865
Patent No. 581768
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNE, JOHN G.
TITLE OF INVENTION: GRAH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOWAS P.
REGISTRATION NUMBER: 38,548
REPERENCE/POCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 544 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                   USA
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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                                                                                                  427 KİTQDELSKVVDNYELLKHSKANVTNSLDKLISSV----SAFTSSNDSKNVLVAPTSMLDQ 482
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                     382 -----READFAKEVPNYKATKDEKIEEIIG--QNGERITSKQV-----DDLIAKGNG 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                | | | : :: | | | :: | | | 427 KITQDELSKVVDNYELLKHSKOVTNSLDKLISSV----SAFTSSNDSRNVLVAPTSMLDQ 482
TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                                                                                                 183 IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANQ 242
                                                                                                                                   VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE 311
                                                                                                                                                                                                     PAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL 371
                                                                                                                                                                                                                                                                       372 VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
                                                                                                                                                                                                                                                                                                                                          432 KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS 491
                                                                 AKGFSNICNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/09124491
) Patent No. 602260
) GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
ITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                539 YINKLKFGR-VKNWQVTDGEASSKLDFS 565
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FILING DATE:
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
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APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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73 VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
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                                                                                                                                                                                                                                                                                                                                                                                                    81; Gaps
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                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                             Query Match 19.5%; Score 904.5; DB 3; Best Local Similarity 38.7%; Pred. No. 1.9e-62; Matches 220; Conservative 98; Mismatches 169;
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REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
TELEPRA: (415)327-3431
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09383912
Patent No. 6521746
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRAH-LEUKOTOXIN CHI
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEB: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 20
CITY: PALO ALTO
                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                  TYPE: amino acid
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COUNTRY: L
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US-09-383-912-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
19.5%; Score 904.5; DB 4; Length 544;
Best Local Similarity 38.7%; Pred. No. 1.9e-62;
Matches 220; Conservative 98; Mismatches 169; Indels 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 YAERFKKLGYDGDNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAN--
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                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
UNRRENT APPLICATION DATA:.
APPLICATION NUMBER: US/09/383,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 YINKLKFGR-VKNWQVTDGEASSKLDFS 565
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: WCCRACKEN, THOMAS P.
NAME: WCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION:
TELEPHONE: (415)327-3400
TELEPRAK: (415)327-3321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSSLOFARGSOHWSYGLRPGSGSODWS
                                                                                                                                                           CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-09-383-912-10
COMPUTER READABLE FORM:
                                                                                                                                          FILING DATE:
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Search completed: February 17, 2004, 10:11:33

Job time : 29 secs

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February 17, 2004, 10:12:24 ; Search time 39 Seconds (without alignments) 4976.856 Million cell updates/sec
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1 MSNINVIKSNIQAGLNSTKS.....SSNALQPITQPTQGILAPSV 927
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| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 4642 99.9 927 11 US-09-884-696-2 Sequence 2, Appli 3 2236.5 48.1 956 11 US-09-884-696-5 Sequence 2, Appli 4 1845 39.7 1023 11 US-09-884-696-5 Sequence 3, Appli 6 408.5 8.8 1115 15 US-10-193-950-5 Sequence 2, Appli 6 408.5 8.8 1115 15 US-10-193-950-5 Sequence 2, Appli 7 295.5 6.4 10.7 12 US-10-306-9493-10178 Sequence 2.106 No. 10 230.5 5.0 1778 12 US-10-369-493-10178 Sequence 2016 No. 10 230.5 5.0 1778 12 US-10-369-493-20175 Sequence 20178, Appli 12 226.5 4.9 212 10 US-09-312-144-9 Sequence 2, Appli 12 22.5 4.9 212 10 US-09-312-183A-2 Sequence 2, Appli 13 216 4.7 2285 10 US-09-312-183A-2 Sequence 2, Appli 13 216 4.7 2285 10 US-09-32-183A-2 Sequence 2, Appli 14 211.5 4.8 2039 15 US-10-192-584-7 Sequence 7, Appli 15 202 4.3 2333 10 US-09-312-183A-2 Sequence 2, Appli 15 202 4.3 2333 10 US-09-797-662-33 Sequence 33, Appli 15 202 4.3 2333 10 US-09-797-662-33 Sequence 33, Appli 15 202 4.3 2333 10 US-09-797-662-33

Sequence 19032, A	Sequence 1, Appli	Sequence 4, Appli	4	Sequence 3, Appli		m	Sequence 12610, A	Sequence 19792, A	Sequence 32, Appl	Sequence 11, Appl	Sequence 28, Appl	Sequence 257, App	Sequence 12996, A	Sequence 19046, A	Sequence 20095, A	Sequence 20096, A	Sequence 6, Appli	Sequence 57, Appl	Sequence 55, Appl	Seguence 5835, Ap	Sequence 68, Appl	Sequence 2, Appli	Sequence 522, App	Sequence 63, Appl	٠.	Sequence 14403, A	Sequence 252, App	Sequence 2, Appli	Sequence 45, Appl
US-10-369-493-19032	US-09-841-786-1	US-10-175-275-4	US-10-175-282-4	US-10-175-275-3	US-10-175-282-3	US-09-815-242-5639	US-09-815-242-12610	US-10-369-493-19792	US-09-797-862-32	US-10-185-990-11	US-10-311-879-28	US-10-114-170-257	US-09-815-242-12996	US-10-369-493-19046	US-10-369-493-20095	US-10-369-493-20096	US-09-841-786-6			US-09-815-242-5835	US-09-971-536-68	US-09-117-447-2	US-09-882-227-522	US-10-193-764-63	US-10-369-493-11841	US-10-369-493-14403	US-10-085-959-252	US-10-092-880-2	US-10-193-764-45
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APPLICANT: ANGELOS, JOHN A
APPLICANT: HESS, JOHN F
TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
TITLE OF INVENTION: AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
TITLE OF INVENTION: BOVIS INPECTIONS
FILE REPRESENCE: 401.06
CURRENT APPLICATION NUMBER: US/09/884,696
CURRENT FILING DATE: 2001-06-19
NUMBER: OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VET: 2.1
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Sequence 2, Application US/09884696
Publication No. US20030035809A1
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 926; Conservative
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, ORGANISM: Moraxella bovis
US-09-884-696-2
                                                                      APPLICANT: GEORGE, LISLE W
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| Publication No. US20030035809A1
| GENERAL INFORMATION |
| APPLICANT: GENERE, LISLE W
| APPLICANT: ANGELOS, JOHN A
| APPLICANT: HESS, JOHN A
| APPLICANT: HESS, JOHN A
| APPLICANT: HESS, JOHN A
| TITLE OF INVENTION: MORAKELLA BOVIS CYTOTOXIN GENE, ANTIBODIES
| TITLE OF INVENTION: AND VACCINES FOR PREVENTION AND TREATMENT OF MORAKELLA
| TITLE OF INVENTION: BOYIS INFECTIONS
| FILE REFERENCE: 481.06
| CURRENT APPLICATION NUMBER: US/09/884,696
| CURRENT FILING DATE: 2001-06-19
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PATENTING TO SECTION OF SEQ ID NOS: 41
| SOFTWARE: PATENTING TO SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF
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SQLAKLGSTISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGK
                     KVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAA
                                                                                               KVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAA
                                                                                                                                                       DKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAV
                                                                                                                                                                                                                                 GSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYD
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                                                                                                                                                                                                                                                                                                           SRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADA
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                                                                                                                                                                                                383 ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL
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                                                                            AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS
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                                                         8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET
                             26;
 Length 953
                             Indels
50.0%; Score 2325; DB 11; 49.9%; Pred. No. 2.5e-158;
                             Matches 464; Conservative 175; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVGSMALFGTANSVSSNALQPITQPTQGI 922
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Sequence 5, Application US/09884696
| Sequence 5, Application US/09884696
| Sequence 5, Application No. US20030035809A1
| GENERAL INPORMATION:
| APPLICANT: GEORGE, LISLE W
| APPLICANT: ANGELOS, JOHN A
| APPLICANT: HESS, JOHN A
| TITLE OF INVENTION: MORAKELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
| TITLE OF INVENTION: MOYAS INPECTIONS
| TITLE REPERENCE: 481.06
| CURRENT FILING DATE: 2001-06-19
| NUMBER OF SEQ ID NOS: 41
| SOFTWARE: PATENTIN Ver. 2.1
| SEQ ID NO 5
| LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 TFQNFLGTALSSMKIDELIKKQKSGGNVSSSELAKASIELINQLV-DTAASLNNVNSFSQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLAKIGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGK 240
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     DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVK 805
                                                                                                                                  RNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKD 861
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                                                                                                                                                                                                                          Indels
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Similarity 41.8%; Pred. No. 9.2e-124;
11; Conservative 156; Mismatches 311;
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; ORGANISM: Escherichia coli
US-09-884-696-5
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Best Local Simil
Matches 421; C
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Sequence 4, Application US/09884696;
Publication No. US20030038809A1
GENERAL INFORMATION:
APPLICANT: GEORGE, LISLE W
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN B
TITLE OF INVENTION: MOUVECINES FOR PREVENTION AND TREATMENT OF MORAXELLA
TITLE OF INVENTION: BOVIS INFECTIONS
TITLE OF INVENTION: BOVIS INFECTIONS
CURRENT APPLICATION NUMBER: US/09/884,696
CURRENT APPLICATION NUMBER: US/09/884,696
CURRENT PILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 41
SEQ ID NO 4
LENGTH: 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NSTKSGLKNLYLAIPKDYDPQ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ 96
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                                                                                                                                                                                                                                                                                                                                                                      DB 11; Length 956;
                                                                                                                                                                                                                                                                                                                                                                    Query Match 48.1%; Score 2236.5; DB 11; Length Best Local Similarity 47.7%; Pred. No. 5.8e-152; Matches 453; Conservative 188; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumoniae
US-09-884-696-4
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                             | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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FEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGK 536
                                                                                                  YSYINKLKFGRUKNWOVTD-GEASSKLDFSKVIQRVAETEGT-DEIGLIVNAKAGNDDIF 594
                                                                                                                                                                                                    VGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKVARGD--IYHEVV 651
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APPLICANT: Jack G. Manns
APPLICANT: Stephen D. Acres
APPLICANT: Stephen D. Acres
APPLICANT: Stephen D. Acres
TITLE OF INVENTION: WITHOUS OF RAISING ANIMALS FOR MEAT PRODUCTION
FILE REFERENCE: 9001-0048
CURRENT APPLICATION NUMBER: US/09/305,924A
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: US 60/084,217
EARLIER FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
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ORGANISM: GnRH
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Sequence 2, Application US/10193950A;
Publication No. US20030104002A1
GENERAL INFORMATION:
APPLICANT: Sparling, P. Frederick
APPLICANT: Thompson, Stuart
TITLE OF INVENTION: Antigenic iron repressible proteins from N. meningitidis related
TITLE OF INVENTION: Antigenic iron family of toxins
FILE REFERENCE: 381-39 CIP/CONII/CPA/CON
CURRENT APPLICATION NUMBER: US/10/193,950A
CURRENT FILING DATE: 1998-03-20
FRIOR FILING DATE: 1998-03-20
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: PAECHLIN Version 3.1
SEQ ID NO 2
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                                                                                                                                                                                              QVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALD 310
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285 NIKCLGTLCDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELAN 344
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                                                                                     QAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSN
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952 DALNGGEGNDHLNGEDGNDTLIGGAGNDYLEGGSGSDTYVFGEGFGQDTVXNYHVDKNSD 1011
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                           292 RSGKYHVYDPLALDLDGDGIETVAAKGFA-----GALFDHRNQGIRTATGWVSA-DDG 343
                                                        229 FALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIM 288
                                                                                   344 LLVRDLN------GNGIIDNGAELFGDNT---KLADGSFAKHGYAALAELD-- 385
                                                                                                                289 LAISPLAFMNAADKFNHANALDEFAKQFRKFGYDG----DHLLAEYQRGVGTIEASLTTI 344
                                                                                                                                           ----SNGDNIINAADAAFQTLRVWQDLNQDGISQANELRTLEELGIQSLDLAYKDV 437
                                                                                                                                                                        345 STALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILE 404
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; Sequence 20166, Application US/10369493 ; Publication No. US20030233675A1 ; GENERAL INFORMATION:

US-10-369-493-20166

APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J.

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Q
                                    APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10(52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 20166
LENGTH: 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.4%; Score 295.5; DB 12; Length 1017; Best Local Similarity 22.6%; Pred. No. 2.5e-12; Matches 182; Conservative 92; Mismatches 282; Indels 249;
                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(1017)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                        ORGANISM: No. US20030233675Altoc punctiforme
Slater, Steven C
Goldman, Barry S
Chen, Xianfeng
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APPLICANT: I.N.S.E.R.M.

TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei
FILE REFERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT APPLICATION NUMBER: 0003145
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
SOFTWARE: Patentin version 3.1
SEQ ID NO 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3975
                                                                                                                                                                                                                                                                                        |::|:|: | : : | | : : | | | : : | | | 3776 ASDLTIDSAQVAGQTLDMSGAGNVTVSLASATTASYSSLTSTGAGTLGLQIGSTGTYT-- 3833
                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 TDTSSNIQGSTFSALVTÅGADÅTYLDATDDILTVTAAQÅATTNINFTAADVVTVSDTGSN 3685
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                                                                                     -----TGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 749, Application US/10238075; Publication No. US20030148324A1; GENERAL INFORMATION:
    ------STALGAVSAGVSA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-10-238-075-749
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Salete, Gregory J.
APPLICANT: Salete, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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                               DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDK-- 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOUGATION: (1)..(4327)
; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-10178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: magnetite-containing magnetic coccus
                                                                                                                  986 GLYGGLSFGQLSFSGNNILVTSTNE 1010
                                                                                         783 ----LAFADANIS--DIMIERTKE 800
                                                                                                                                                                                                                                         Sequence 10178, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (1)..(4:
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PLANTS FOR PRODUCTION

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MICROBIAL PROTEINS

Slater, Steven Goldman, Barry Chen, Xianfeng

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                          GDRSM--AFGRYAKTNGFTSLAIG----DSSLADGEK------TIALGNTAKA 184
                                                      TOTIEAFSSOLAKLGSTISOAKGFSNIGNKLONLNFSKTNLGLEIITGLLSGISAGFALA 232
                                                                           YEIMSIALGDNANASKEYAMALGASSKAGGADSLAFGRKSTANS--TGSLA-IGADSSS 241
                                                                                                                                                                     SPLAF-MNAADKFNHANALDE------FAKQFRKFGYDGDHLLAEYQRGVGTIEA 339
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RESULT 10
US-10-369-493-20175
Sequence 20175, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

APPLICANT: Cao, Yongwei APPLICANT: Hinkle, Gregory J.

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APPLICANT: Tucker, Kenneth
APPLICANT: Tucker, Laura
APPLICANT: Plosila, Laura
TITLE OF INVENTION: MORAXELIA CATARRHALIS OUTER MEMBRANE PROTEIN-106 POLYPEPTIDE, GENT
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-089-999
CURRENT APPLICATION NUMBER: US/09/813,214A
CURRENT FILING DATE: 2000-03-20
PRIOR PAPLICATION NUMBER: 08/968,685
PRIOR PILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 20
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23.0%; Pred. No. 3.9e-08;
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US-10-369-493-20175
TITLE OF INVENTION: EXPRESSION OF MICROBIAL E TITLE OF INVENTION: PLANTS WITH IMPROVED PROFILE OF INVENTION: PLANTS WITH IMPROVED PROFILE OF INVENTION NUMBER: US/10/369,493 CURRENT APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374
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Matches 225; Conserv
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US-09-932-183A-2
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US-09-932-183A-2
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| AATIKDLYNLSQVPLTFAG------DTGPNVTKKLGEILKV----
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                                                                                                                                                                                        GINAGGKELTNVQSAI ----NPATNGGQLDFM-------NRLSTANTEKSGS
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                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.9%; Score 226.5; DB 10; Length 2122; Best Local Similarity 20.3%; Pred. No. 6.9e-07; Matches 227; Conservative 130; Mismatches 362; Indels 397;
                                               TYPE: PRT ORGANISM: Moraxella catarrhalis
SOFTWARE: Patentin version 3.0 SEQ ID NO 9
                                2122
                                                                 ; ORGANISM: MUJ
US-09-813-214A-9
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1423 FALSNQATGDALVKASDIVAHLNT----LSGDIQTAKGASQANSSAGYVDADGNKVIYDS 1478
1365 VNF--ADGNATTAKVTYDDTSKTSKVYYDVNVDDTTIEVKDKKLGVKTTTLTSTGTGANK 1422
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                                                                                                                                    -----IVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQ 851
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                                                                                                                                                                                                                                                                                                                                                                                          --- LADENKSQKLS
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larity 20.6%; Pred. No. 2.7e-06;
Conservative 153; Mismatches 375; Indels 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09932183A;
Sequence 2, Application US/09932183A;
Patent No. US20020127641A1
GENERAL INFORMATION:
APPLICANT: Estell, David A.
TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394C1-US
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US/09/302,183A
CURRENT FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1998-09-08
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAOTPL 1574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETTRAFRTFDENKDYMRQAMALGFNAKVSRGKGKMETGINSMAIGARSQATLQNSTALGV 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
4.6%; Score 216; DB 15;
Best Local Similarity 20.2%; Pred. No. 3.7e-06;
Matches 215; Conservative 126; Mismatches 424;
                                                                                                                                                                                                                                                                                                         TOKUNAGA=1
                                                                                                                  FILING DATE: 19-May-1998
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
                                                                                                                                                                                      APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
FILING DATE: 11-Jul-2002
PRIOR APPLICATION DATA:
APPLICATION ...
APPLICATION ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                        NAME: KORNBAU, Anne M.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TO
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVENIDRKLGKASNVLSTL
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 2039 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1216 IDSLKKLRKERKLDMSEAELSDLEVKSINNVADAKKELKKLERKMLQPGGYSNSQIEAMQ 1275
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MATSUO, KAZUO
HAMADI, FAKUSBUTO
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1004 ALDSGDEKAPDNAKKDLOSLLETYSKSDSSIDVFKMSFDKAQKNIKDGDKSLSSVKSEVG 1063
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                                                                                                                                                                                                                                                                                          914 IADDDDYKVAADKAKQSMLKAQSDIESG---NAKVKDSVLSIANAYSSID------ 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIFRKGDG----NDTLYDGTGNDKLA---FADANISDIMIERTKEGIIVKRNDHSGSINIP 816
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                                                                                                                                                                   ELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITL 495
                                                                                                                                                                                              554 TDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELR 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           674 KVGYGYQST-DN----LKSVEEVIGSQFN--DVFK------GSKFNDIFHSGEG 714
                          737 KTALRGLLVSTLVGGAFAALGWALESLISSFAEAKKAKDDFEQSQQTNVEAITTNKDSTD 796
                                                                         -----NGGQNYFD------KGYDSRYAAYLANNLKFLS 435
                                                                                                                                                                                                                                                             496 DAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKY--SYINKLKFGRVKWWQV 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RWYITSNLONYOSNKTDHKIEQLIGKDGSYITSDQI---DKILQDKKDGTVIT----
                                                                                                                    KLIQQYKELQKVKESRSLTSDEEQEYLQVTQQLAQTFPALVKGYDSQGNAILKTN-
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COMPUTER: IBM PC compatible
OPERATION PC-DOS/MS-DOS
SOFTWARE: PATENT IN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10192584
Publication No. US20030027987A1
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
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COMPUTER READABLE FORM:
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COUNTRY: USA
                                                                         KILEWEKQ-
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US-10-192-584-7
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977 AISIGTNSDTSMTGAVAIGKGATVTAGGKPSIALQQDSTVANSAISRT-SSPMINGLIFN 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                         307 NALDEFAKOFRKFGYDGDHLL-----AEYQRGVGTIEASLTTISTALGAVSAGVSAA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          870 LKTTA----SALNQVATQLEQEVTTNNFDKFNQYK-----TQIENASNADSARNVG 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIDGGDGHD-----RVFYSKD-----GGFGNITV--DGTSATEAGSYTVNRKVARGDIYH 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484 TTSAGAIK-----KTATTDSSÄGGGKNAIAIGSK----TFASKANSVALGSYALADAQ 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 KILEWEKQNGGQNYFDKGYDSRYAAYLAN-NLKFLSELN--KELEAERVIAITQQRWDNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 SQSTQTIEAFSSQLAKLGSTISQAKGFSN---IGNKLQNLNFSKTNLGLEIITGLLSGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         533 NAFALGSYSFVESSATNTITIGVGSYAKGKNSFLGGTWASTLSDRTVVLGNSTSISSGSQ
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                                                                                                                                                                                                                                                                                 388 GNKTEASNAGSMAYGYKAKAVGAGAIAIGTEVAAGAKF-NSHQTGNILQDNNAYATLKNA
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                                                                                                                                                                                                                                                                                                                                    61 -NHTETAKKSVDTVNQFLSLTQTGIAISATKL---EKFLQKHSTNKLAKGLDSVENI---
                                                                                                                                                                            DB 15; Length 2042;
                                                                                                                                                                                                                                                         11 IQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP---
                                                                                                                                                                                                                  Indels
                                                                                                                                                                            4.6%; Score 211.5; DB 15;
ilarity 22.0%; Pred. No. 7.8e-06;
Conservative 123; Mismatches 386;
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SEQUENCE CHARACTERISTICS:
LENGTH: 2042 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                              Similarity
                                                                                                                                                                                Local b. 225; C
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US-10-192-584-6
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OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                            987
                                                                                                                                                                              ------KVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYGTDN 684
                                              1046 GVLSIGTAGKERKIVNVAAGDI-----SQTSTEAINGSQLYATNFMLNKLA-----
                                                                                                                                                                                                                                                           LKSVEEVIGSOFNDVFKGS-KFNDIFHSGEGDDLLDGGAGDDRLFGGKGN-----DRLSG
                                                                                                                                                                                                                                                                                                                                      739 DEGDDLLDGGSGDDVLNG-----GAGNDVYIFRKGDGNDTLYDGTGND-KLAFA
                                                                                                                                                                                                                                                                                                                                                                                                                 DANISDIMIERTKEGIIVKRNDHSG-SINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGS
                                                                                                   ---DDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNR
                        NKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 TIDSTTNSAQTNLVKVSRDGF----SVKNGSDESKLASTKLS 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846 YI---TSDQIDKILQDKKDGTVITSQELKKLADENK--SQKLS 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
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FILING DATE: 19-May-1998
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
ATTONEY/AGENT INFORMATION:
NAMB: KORNBAU, Anne M.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/192,584
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REFERENCE/DOCKET NUMBER: TO
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TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATSUO, Kazuo
HAMADA, Fukusaburo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-Jul-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAKAGUCHI, Masashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10192584
Publication No. US20030027987A1
GENERAL INFORMATION:
APPLICANT: TOKUNAGA, Eiji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Qy 762 VYFPKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRUDHSGSINIPRWY 819 Db 1134 IYLKADQNDPTONGGGKVELGNAITLSATNOWA	Query Match 4.3%; Score 202; DB 10; Length 2353; Beef Local Similarity 20.0%; 20.0%; Pred. No. 4.76-05; Most State 129; Mismatches 338; Indels 338; Gaps 48; Autches 212; Conservative 129; Mismatches 338; Indels 338; Gaps 48; 48; Qy 62 4.7%-05; Hill

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818 WYITSNLQNYQSNKTDHK 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 LGKASNVLST-----LSSFLGT-ALAGIELDSLIKKGDAAPDALAKAS--IDLINEII 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNLSQSTQTIEAFSSQLAKLGSTISQAK----GFSNI---GNKLQNLNF----SKTNLG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTKAISSYVLAQRVAAGLSTTGAVA-ALITSSIMLAISPLAFMNAADKFN----HANALD 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAG-----VSAAAVGSAVG 365
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                                                                                                                             GENERAL INFORMATION:
APPLICANT: STEWART, GEORGE C.
APPLICANT: STEWART, GEORGE C.
APPLICANT: STEWART, GEORGE C.
APPLICANT: STEWART, GEORGE C.
APPLICANT: NARAYAMAN, SANJEEV K.
APPLICANT: CHENGAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
FILE REFERENCE: 30296
CURRENT PAPLICATION NUMBER: US/09/841,786
CURRENT PAPLICATION NUMBER: 09/558,257
PRIOR APPLICATION NUMBER: 09/558,257
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVIKSNIQAGLNSTKSG-----LKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
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                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Fusobacterium necrophorum
US-09-841-786-1
                                                                                                        Sequence 1, Application US/09841786 Patent No. US20020054883A1
                         118 GGVGNDIL 125
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APPLICANT: HARKNESS, Robin E.
APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
TITLE OF INVENTION: Michel H.
TITLE OF INVENTION: MORAKELLA
FILE REFERENCE: 1038-1235 MIS
CURRENT APPLICATION NUMBER: 08/425,275
CURRENT APPLICATION NUMBER: 08/431,718
PRIOR PAPLICATION NUMBER: 08/431,718
PRIOR PAPLICATION NUMBER: 08/431,718
PRIOR PAPLICATION NUMBER: 08/431,718
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-03-16
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-03-26
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 4
LENGTH: 1833
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                                                                                                                     ---STTGALVAG---NWEIGD----KLETIARDNTIVRVNGDGTKGGLVGKNGISVKNT 2957
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| : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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535 GKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIV-
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4.2%; Score 197; DB 12;
Best Local Similarity 19.6%; Pred. No. 7.3e-05;
Matches 238; Conservative 157; Mismatches 407;
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| GYD----KNYNISKTNSK 3156
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1038 IIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNF--ADGNATTAKVTYDDTSK 1095
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                                              LKAAKPTLNA------GAGISVTPTEISVDAKSGNVTAPTYNIGVKTTELNSDGTSDK 390
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GENERAL INFORMATION:
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APPLICANT: BASAKI, Ken
APPLICANT: HARKNESS, Robin E.
APPLICANT: COGSMORE.
APPLICANT: CHOOSGORE.
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ITILE OF INVENTION! MORAELLA
FILE REFERENCE: 1038-1234 MIS
CURRENT APPLICATION NUMBER: 08/945,567
FRIOR APPLICATION NUMBER: 08/945,567
FRIOR APPLICATION NUMBER: 08/431,718
FRIOR FILING DATE: 1995-06-01
FRIOR APPLICATION NUMBER: 08/431,718
FRIOR PELING DATE: 1995-06-01
FRIOR APPLICATION NUMBER: 08/431,944
FRIOR FILING DATE: 1996-03-26
FRIOR APPLICATION NUMBER: 08/621,944
FRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 10
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; Sequence 4, Application US/10175282; Publication No. US20030170657A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Moraxella catarrhalis
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Fublication No. US20030171254A1
Sequence 3, Application No. US20030171254A1
GENERAL INFORMATION:
APPLICANT: BASAKI Ken
APPLICANT: LOCSMORE, Sheena M.
APPLICANT: CHONG, Pele H.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
TITLE OF INVENTION: WORAXELLA
FILE REFERENCE: 1038-1235 MIS
CURRENT APPLICATION NUMBER: 08/945,567
FRICK APPLICATION NUMBER: 08/945,567
FRICK APPLICATION NUMBER: 08/945,567
FRICK APPLICATION NUMBER: 08/411,718
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FRICK APPLICATION NUMBER: 08/411,414
FRICK APPLICATION NUMBER: 08/621,944
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                                                                                                                                                                                                                                                      Length 1992;
                                                                                                                                                                                                                                                 Query Match
4.2%; Score 197; DB 12;
Best Local Similarity 19.6%; Pred. No. 8.3e-05;
Matches 238; Conservative 157; Mismatches 407;
PRIOR APPLICATION NUMBER: PCT/CA96/00264
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEQ ID NOS: 10
SCFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 1992
TYPE: PRT
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| Publication No. US20030170657A1
| GENERAL INFORMATION:
| APPLICANT: SASAKI, Ken
| APPLICANT: GASAKI, Ken
| APPLICANT: LOOSMORE, Sheena M.
| APPLICANT: LOOSMORE, Sheena M.
| APPLICANT: LOOSMORE, Sheena M.
| APPLICANT: CLONG, Pele
| TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
| TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
| TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
| TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
| TITLE OF INVENTION: UNGRER: US/10/175,282
| CURRENT APPLICATION NUMBER: US/405/567
| PRIOR APPLICATION NUMBER: 08/431,718
| PRIOR APPLICATION NUMBER: 08/431,718
| PRIOR APPLICATION NUMBER: 08/431,718
| PRIOR FILING DATE: 1995-06-07
| PRIOR FILING DATE: 1995-06-07
| PRIOR FILING DATE: 1996-04-29
| WINDER OF SEQ ID NOS: 10
| SEQ ID NOS: 10
| SEQ ID NOS: 10
| SEQ ID NOS: 10
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                                           1197 IIKDEDKTRAASIVDVLSAGFNLQGNGEAVDFVSTYDTVNF--ADGNATTAKVTYDDTSK 1254
                                                                                                                                                                                      814 NIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQID-KILQDKKDGTVITSQELKK 872
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                                                                                          ---DVYIFRKGDGNDT----LYDGTGN 780
                                                                                                                                                               -----IVKRNDHSGSI 813
                                                                                                                                                                                                                                                                                                            ---LADENKSOKLSASDI----ASSLNKLVGSM 898
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4.2%; Score 197; DB 12; Length 1992;
Best Local Similarity 19.6%; Pred. No. 8.3e-05;
Matches 238; Conservative 157; Mismatches 407; Indels 412;
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                                                                                                                                                               781 DKLAFADANISDIMIE--RTKEGI-------
                                                                                          DLLD----GGSGDDVLNGG---AGN---
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ORGANISM: Moraxella catarrhalis
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US-10-175-282-3
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-----IVKRNDHSGSI 813

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1437 RISIQNDNITKTSQNYLDASDSNKNNYNTAVNNANGVINVTNNPNMDANAINGMANQVNT 1496
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                                                      1038 VAGVDTVKSSANTLNGAMGTLRNSIODNTATNNGONYLDATESNKTNYNNAVDSANGVIN 1097
                                                                                                                                                                                    098 ATSNPNMDANAINQIATQVTSTKNALDGTHNLTQAKQTATNAIDGATNLNKAQKDALKAQ 1157
                                                                                                                                                                                                                                                                                                                      1158 VTSAORVANVTSIOOTANELNTAMGOLOHGIDDENATKOTOKYRDA-EOSKKTAYDQAVA 1216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITVDGTSATEAGSYTVN-----RKVARGDIYHEVVKRQ-----
-KILEWEKQNGGQNYFD-
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Patent No. US/2020661569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Tyskind, Judith W.
APPLICANT: Trawick, John D.
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PRIOR APPLICATION NUMBER: 60/191,078
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Carr, Grant J.
Yamamoto, Robert T.
----FESVANRLQG----
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4.2%; Score 196; DB 9; Length 2086;
Best Local Similarity 18.6%; Pred. No. 0.0001;
Matches 221; Conservative 165; Mismatches 431; Indels 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Essential Genes
                                                                                                                                                                                                               APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Tayskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Tentification of Essent:
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
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TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: PROKARYOTE
TITLE OF INVENTION NUMBER: US/09/815,242
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5639
                                                                                               5639, Application US/09815242 or US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5639
                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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; Sequence 19792, Application US/10369493
; Publication No. US20030233675A1
                                                                                                                                                                       662 TETIQ-----YRD-YELRKVGY
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Best Local Similarity
Matches 70; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 ----IEASLTTISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAM- 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 LGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQS---- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 ---TQTIEAFSSQLAKGGSTISQAKGFSNIGNKLQNLNFSKTNL--GLEIITGLLSGISA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GFALADKNASTGKKVAAGFELSNQVIGNVT-----KAISSYVLAQRVAAG---LSTTG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 AVAALITSSIMLAISPLAFMNAADKFNHANALDEPAKQFRKFGYDGDHLLAEYQRGVGT- 336
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
4.2%; Score 196; DB 9; Length 5795;
Best Local Similarity 18.6%; Pred. No. 0.0005;
Matches 221; Conservative 165; Mismatches 431; Indels 372;
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-3
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SOFTWARE: PRESENTION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
SOFTWARE: PRESENTION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
SOFTWARE: PRESENTION NUMBER: 60/269,308
FRIOR FILING DATE: 2001-02-16
SOFTWARE: PRESENTION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Staphylococcus aureus US-09-815-242-12610
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Gladen, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19792
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FSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKD--GGFGN
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Qy 469ERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQ 513	Qy 514	OY 555 DGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKWNIDGGDG 607	Qy 661 RTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSG 712		Qy 772 DTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSN 823	Qy 824 LQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQD 858 :	859VITSQB		:: 1047 MVA	RESULT 26 US-10-185-990-11 ; Sequence 11, Application US/10185990 ; Publication No. 18200307310941	GENERAL INFORMATION: ; APPLICANT: Pan, Jae-Gu ; TITLE OF INVENTION: JAE GU PAN ET AL	FILE REFERENCE: 02589.000100 ; CURRENT APPLICATION NUMBER: US/10/185,990 ; CURRENT FILING DATE: 2002-06-28 ; NUMBER OF SEQ ID NOS: 11	; SOTTWARE: Patentin version 3.1 ; SEQ ID NO 11 ; LENGTH: 1626 ; TYPE: PRT	SM: Bacillus subtilis 990-11	Query Match 4.0%; Score 188; DB 15; Length 1626; Best Local Similarity 20.2%; Pred. No. 0.00027; Matches 185; Conservative 112; Mismatches 333; Indels 286; Gaps 39	Qy 63 TETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASN 122	CONTRACTOR OF THE CONTRACTOR O
704 KFNDIFHSGEGDDLLDGCAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY 763 :	764 IFRKGDGNDTLYDGTGNDKLAFADANI 790 ::	:SULT 25 :-09-797-862-32 Sequence 32, Application US/09797862 Patent No. US20020102276A1 GENERAL INFORMATION: APPLICANT. PRAK. TAN RICHARD ANSELM	HZUUF	VI AFFILATION NUMBER: US/09/79/79/79/79/79/79/79/79/79/79/79/79/79	G DATE: 1997-12-12 EQ ID NOS: 33 atentIn Ver. 2.1	; SEQ ID NO 32 ; LENGTH: 1098 ; TYPE: PRT ; ORGANISM: Haemophilus influenzae	<pre>562-32 ch 4.1%; Score 188.5; DB 10; Length 1098; al Similarity 19.7%; Pred. No. 0.00014; 225; Conservative 156; Mismatches 389; Indels 373; Gaps 59;</pre>	5 NVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTE 64 : :	65 TAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ-KHSTNKLAKGLDSVENIDRKLGKA 120	121 SNVLSTLSSFLGTALAGIELDSLIKKGDAPDALAKASIDLĮNEIIGNLSQSTQTIEAFS 180 	181 SQLAKIGSTISQAKGFSNIGNKLQULNFSKTNLGLEI 217	218 ITGLLSGISAGPALADKWASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTT- 276 267KGVKAGSTTGQSENVDFVHTYDTVEFLSADTETTT 301	277GAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFG 320	IEASLITISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGL 	VDGANATEDADEGKGLVTAKDVIDAVNKTGWRIKTTDANGQNGDFATVASG 393 ISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDK 417	GTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKN	GIUSKIAATLANNILKFUSELINKELEAEKTAIIQQKRUNNIGELAGIIALG

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997 GFRSTLIAGA---GSVQLAGDRSRLIAGADS-----NQTAGDRSKLLAGNNSYLTAGD 1046
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                                                                                             GERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNG---KKTQALHFTSPLLTA 524
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YESTLTAGYGSTQTAQE-NSSLTTGYGSTSTAGFAS-SLIAGYGSTQTAGYKSTLTAGYG 879
                        STQTIEAFSSQLAKLGSTISQAKGFSNI---GNKLQN--LNFSKTNLGLEIITGLLSGIS 226
                                                 STOTAEYGSSLTAGYGSTATAGODSSLIAGYGSSLTSGIRSFLTAGYGSTLIAGLRSVLI 939
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1107 RYRQLVARTGENGVEADIPYYVNEDDDIVDKPDEDDDWIEVKPGMGVFD-----
                                                                           AGFAL-------ADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAA
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Publication No. US20030186275A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
TITLE OF INVENTION: Antigenic Peptides
FILE REFERENCE: toxin
CURRENT APPLICATION NUMBER: US/10/311,879
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 28
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                                                                                                                                                                                                                                                                                                                                                                                        143 LIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAF---SSQLAKLGST--ISQAK--G 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | : | : | HIT-----TAQRNDLTNQISQATNLAGVESV-------
                                                                                                                                                                            2006 KOOLNNMTHLTTAQKTNLTNQINSGT---TVAGVQTVQSNANT---LDQAMNTLRQSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2060 KDATKASEDYVDANNDKQTAYNNAVAAAETIINANSNPEMNPSTITQKAEQVNSS----
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                                                                                                                                                     4 INVIKSNIQAGLNSTKSGLKNL----YLAIPKDY---DPQKGGTLNDFIKAADELGIAR
                                                                                                                                                                                                                                LAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATK----LEKFLQKHSTNKLAKGLDSV
                                                                                                                                                                                                                                                                                                           111 ENIDR-----KLGKASNV----LSTLSSFLGTALAGIE------LDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 FSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGN
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                                                                      ch 4.0%; Score 186.5; DB 12; Length 2659;
al Similarity 19.0%; Pred. No. 0.00073;
186; Conservative 129; Mismatches 353; Indels 309; Gaps
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-311-879-28
                                                                          Query Match
Best Local S:
Matches 186
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                  STQTIEAFSSQLAKLG---STISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAG 228
                                                                                                                                                                                                                                                        285 SSIMLAIS-PLAFMNA-----ADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGT- 336
                                                                                                                                                                                                                                                                                                                                                                     337 IEASLTTISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVAN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 RLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKE----LEAERVIAITQQ 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 EGDDLLDGGSGDDVLNGGAGND------VYIFRKGDGNDTLYDGTGNDKLAFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 RWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSN--GK
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                                                                           ----ivDKFLGGi---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 KTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQR
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                                                                           ----ARMIKMNDNISAIDHAGAVSDIKN---
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Patent No. US20020061569A1;
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel I.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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                                                                                                                                                                                                                                                                                   Burland, Valerie
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. US20030023075Alel Sequences of E. OVERSPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.0%; Score 186.5; DB 15; Length Best Local Similarity 19.4%; Pred. No. 0.00096; Matches 214; Conservative 152; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPHONE: (608) 251-9166
INFORMATION FOR SEQ ID NO: 257:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.4
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
ANAME: 60/110,955
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO: 257:
US-10-114-170-257
                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                                                                                                                                                      Sequence 257, Application US/10114170 Publication No. US20030023075A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
|| : |:|
2521 TPQKAKLKEQVGQANRL 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                   RESULT 28
US-10-114-170-257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GLDSVENIDRKLGKASNVLS-----TLSSFLGTALAGI-----ELDSLIKKGDAAPDA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TAVENALSQVANAKGALNGNHNLEQAKSNANTTINGLQHLTTAQKDKLKQQVQQAQNV 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ----LAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---FSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAQRVAAGLSTTGAVAALITSSIMLAISPL----AFMNAADKFNHANALDEF--AKQFR 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFGYD----GDHLLAEYQRGVGTIEAS-----LTTISTAL-GAVSAGVSAAAVGSAVG 365
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APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: ELITRA.011A
CURRENT FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-0-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PERSERE FOR WINDOWS VERSION 4.0
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JS-09-815-242-12996
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ORGANISM:
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Sequence 19046, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Gladman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
; TITLE OF INVENTION: UNMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 190466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1022 KNSSOTLNTAMKGLRDSIANEATIKAGONYTDASPNNRNEYDSAVTAAKAIINQTSNPTM 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : | : | : | 1.
.082 EPNTITQVTSQVTTKEQALNGARNIAQAKTTAKNNINNITSINNAQKDALTRSIDGATTV 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1142 AGVNQETAKATELNNAMHS-----LONGI------NDETQTKQTQKYLDAEPSKK 1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : : :| | | | :| | 334 EAKAAAKQTLGTLT-HINNAQRTALDNEITQATNVEGVNTVKAKAQQLDGAMGQLETSIR 1292
                                            ----TVDGTSAT 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    858 DKKDGTVITSQELKKLADENK---SQKLSASDIASSLNKLVGSMALFGTANSVSSNALQP 914
513
                                                                                                                                                                                                    846 AALINGAQNIAQAKTINATNTIINNAHDLNQKQKDALKTQVNNAQRVSDANNVQHTATELNSA 905
                                                                                                                                                                                                                                                                              562 LDFSKVIQRVAETEGTDEIGLIVNA-----KAGN------DDIFVG
                                                                                                                                                                                                                                                                                                                                                906 MTALKA--AIADKERTKASGNYVNADQEKRQAYDSKVTNAENIISGTPNATLTVNDVNSA
                                                                                                                                     514 -ALHFTSPLLTAGTESRERLTNG------KYSYINKLKFGRVKNWQVTDGEASSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631 EAGSYTVN--RKVARGDIYHEVV-------KRQE-----
----KSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNS---
                                                                                                                                                                                                                                                                                                                                                                                                                          597 QGKMNID----GGDGHDRVFYSKDGGFGNI------
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Q

14; 634

Gaps

88;

81;

Query Match 3.9%; Score 180; DB 12; Best Local Similarity 24.1%; Pred. No. 4.5e-05; Matches 68; Conservative 45; Mismatches 81;

; TYPE: PRT ; ORGANISM: No. US20030233675Altoc punctiforme US-10-369-493-20095

Length 210; Indels 751

694

----SGSNNL-----LGG 70

25

575 EGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGS

635 YTVNRKVARGDIYHEVVKRQETKVGKRIETIQYRDYELRKVGYGYQSTDNLKSVEEVIGS

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695 OFND---VFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGD

805 KRNDHSGSINIPRWYITSNLONYQSNKT-----DHKIEQLIG 841

DVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADAN-----ISDIMIERTKEGIIV 804

APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFRENCE: 38-10(5202.)B
CURRENT FILING DATE: 2002-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

Cao, Yongwei Hinkle, Gregory J. Slater, Steven C.

APPLICANT: (APPLICANT:

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SEVEWVSFSPD------GKIIASASADKTIRLWDSFSGNLIKSLPAHNDLVYS 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIF 765
                                                                                                                                                     149 AAPDALAKASIDLINEIIGNISQSTQTIEAFSSQLAKLGSTI------SQAKGFSNIG 200
                                                                                                                                                                                                                                201 NKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFEL----SNQVIGNV 256
                                                                                                                                                                                                                                                        443 QEFIGACLAERKHQQLQAKNRLKQAQRAVVALSVLGIAS------VSFGGLAYWQGRE 494
                                                                                                                                                                                                                                                                                                                                                                                  - KFNHANALDEFAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAGVSAA-A 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 VGSAVGTPIALLVAGVTGLISGILEASKQAMFE-SVANRLQGK---ILEWEKQNGGQNYF 415
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                         TKLEKFLOKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGD 148
                                                                                                            -----VEQTINVLTNAKLVVINLEAEI---- 349
                                                                                                                                                                                       ---EAQGKS----FSPTPPNLSTPFVTVEVAHEILIRHWSTLRWWLEENRDRLRKQRQIN 402
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KDYDPOKGGTLNDFIKAADELGIARLAEE--PNHTETAKKSVDTVNOFLSLTQTGIAISA 88
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfenn
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US(10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PRILING DATE: 2002-228
PRIOR PRILING DATE: 2002-222
-----GGIGVTQFSALTLLQ--QGSDTLVKAGNTELASLVG 209
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; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20096
                                                                                                                                                                 ; Sequence 20096, Application US/10369493 ; Publication No. US20030233675A1
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SEQ ID NO 20096
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US-10-369-493-20095 ; Sequence 20095, Application US/10369493 ; Publication No. US20030233675A1

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                                                    233 HADNVNMEATHKMKVTAVSKAVTGSVLGGVGVTKAEATAAGKTMVEVEEGNLFRTNRLINA 292
                                                                                                                  411
                                                                                                                                              470 RIKSGKAYADAFEDGKKVEAGSNIT-LDAKTGIIDISNSNGKKTQALHFTSPLLTAGTES 528
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HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAG-----VSAAA 359
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                                                                                                               360 VGSAVG-----TPIALLVAGVTGLI--SGILEASKQAMPESVANRLQGKILEWEKQNGG
                                                                                                                                                                                                                                 412 QNYPDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGEL--AGITKLGE
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APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: MOLECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECTIAR WEIGHT PROTEINS
TITLE OF INVENTION: MOLECTIAR WEIGHT PROTEINS
CURRENT APPLICATION NUMBER: US/10/193,764
CURRENT APPLICATION NUMBER: US/10/193,764
FRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
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669 NINVYAGYD----KNYNISKTNSK 688
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; ORGANISM: Haemophilus influenzae
US-10-193-764-57
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SEQ ID NO 57
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                                                                                                                                                                                                                                                                                                  ----LKPNQTLFAGD 118
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Patent No. US2002005488341

GENERAL INFORMATION

APPLICANT: NGARAJA, T. G.

APPLICANT: STEWART, GEORGE C.

APPLICANT: TARATANAN, SANJEEV K.

APPLICANT: CHENGAPPA, M. M.

TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN

TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF

FILE REFERENCE: 30296

CURRENT APPLICATION NUMBER: US/09/841,786

CURRENT APPLICATION NUMBER: US/09/841,786

FRIGH STATIST OF DATE: 2001-04-24

PRIOR FILING DATE: 2000-04-25

FRIENCE FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                            GTDE1----GLIVNAKAGNDD1FVGQGKWNIDGGDGHDRVFY-----SKDGGFGNI
                                                                                                                     GELAG--ITK-LGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQAL
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                                                                                                                                                                            GDLKGRAİTEALGGRPGCSSLYXRSI-DFEKTTNGQATVLDSQS----VGNTQ-----
                                                                                                                                                                                                                                    HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETE
                                                             Gaps
; Score 180; DB 12; Length 273;
; Pred. No. 6.7e-05;
37; Mismatches 100; Indels 116;
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      3.9%;
Query Match
Best Local Similarity 25.8*
Matches 88; Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 773
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                                                                                                      RKFGYDGDH--LLAEYORGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALLVAG 374
                                                                                                                                           VTGLISGILEASKQAMFESVANRLQ-----GKILEWEKQNGGQNYFDKGYDSR 422
                                                                                                                                                             -----SFKAKNDTNHANQLPIQFNSNISVDGGGKVLFCITSNYSGRSVGIGMSSI 333
                                                                            694 ITSNKTV-NITASEKLTTKADATINATTGNVEVTAKTGDIKGEVKST--SGNVNITANGD
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                                             NITAKGSIAFE-----GNGTEKARNASSAQITAQGTITNTGDQKQLRLNNVSINGTGIG
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llarity 22.2%; Pred. No. 0.00057;
Conservative 110; Mismatches 329;
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 998
                                                                                                                                                                                                                                                                                         ; ORGANISM: Haemophilus influenzae
US-10-193-764-55
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Matches 207; Conserv
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OY 881 KLSASD1ASSLNKLVGSMALFCTANSVSSN 910	OV 249 SNOVIGNUTKAISSYVLAORVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD 301
793	: 1352 NNAQSTAAT
RESULT 36	302 KENHANALDEGTIEASLTTIS
US-09-815-242-5835 ; Sequence 5835, Application US/09815242	Db 1392 GINDQNTVKQQVNFTDADQGKKDAYTNAVTNAQGILDKAHGQNMTKAQVEAALNQVT 1448
Patent No. US20020061569A1	Qy 346 TALGAVSAGVSAAGSAVGTPIALLVAGVTGLISGILEASKOA 389
APPLICANT: Haselbeck, Robert	Db 1449 TAKNALNGDANYRQAKSDAKANLGTLTHLNNAQKQDLTSQIBGATTVNGVNGVKTKAQ 1506
; APPLICANT: Ohlsen, Karl L. ; APPLICANT: Zyskind, Judith W.	Qy 390 MFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLS 435
; APPLICANT: Wall, Daniel : APPLICANT: Trawick John D	1507
CANT: Yamamoto, Robert T. CANT: Xu, H. Howard	436 ENIGE-LAGITK : :: : : :: :
<pre>; TITLE OF INVENTION: Identification of Essential Genes in ; TITLE OF INVENTION: Prokaryotes</pre>	Db 1567 EQAIQSVTSTENALNGDANLQRAKTEAIQAIDNLTHLNTPQKTALKQQVNAAQRVSGVTD 1626
; FILE REFERENCE: ELITRA.011A : CURRENT APPLICATION NUMBER: US/09/815.242	Oy 467 LGERIKSGKAYADAFEDGKKVEAGS-NIT 494
CURRENT FILING DATE: 2001-03-21	Db 1627 LKNSATSLNNAMDQLKQAIADHDTIVASGNYTNASPDKQGAYTDAYNAAKNIVNGSPNVI 1686
PRIOR FILING DATE: 2000-03-21	Qy 495 LDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVT 554
	Db 1687 TNAADVTAATQRVNNAET-GINGDTNLATAKQQAKDALRQMT 1727
AFFLICATION NUMBER: 60/20/,/2 FILING DATE: 2000-05-26	QY. 555 DGBASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNID 603
APPLICATION NUMBER: 60/242,57 FILING DATE: 2000-10-23	DD 1728 HLSDAQKQSITGQIDSATQVTGVQSVKDNATNLDNAMNQLRNSIANKDDVKASQPYVD 1785
; PRIOR APPLICATION NUMBER: 60/253,625 : PRIOR FILING DATE: 2000-11-27	OV 604 GGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKROET 656
	1786 ADRDKONAYNTAVINAENIINATSOPTLDPSAVTOAANOVSTNKTALNGAONLANKKOET 1
; PRIOR APPLICATION NUMBER: 60/269,308 ; PRIOR FILING DATE: 2001-02-16	KVGKRTETI OYRDYELRKVGYGYOSTDN
24.43	1846 TANINQLSHLMNAQKQDLMTQVTNAPNISTVNQVKTKAEQLDQAMERLINGIQDKDQ
۵.: ت. ع	Qy 685 LKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGA 722
TYPE: PRT ORGANISM: Staphylococcus aureus	: : : 1903 VKQSVNFTDADPEKQTAYNNAVTAAENIINQANGTNANQSQVEAALSTVTTKQALN 1959
	Qy 723 GDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGND 761
atch 3.8%; Score 177.5; DB 9; Length 2434; cal Similarity 17.9%; Pred, No. 0.0028;	
Gaps	Qy 762 VYIFRKGDGNDTLYDGT-GNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRW 818
Qy 2 SNINVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADEL 51	Db 2019LKNSLNDKDTTLGSQNFADABEKKNAYNEAVHNAENILNKSTGTNVPKD 2068
52GIARIAERDNHTETAKKSUDTUNOFISITO	Qy 819 YITSNLQNYQSNKTDHKIEQLIGKDG-SYITSDQIDKILQDKKDGTVITSQ 868
1057 NDNKAAVEQALQRVNTAKTALNGDERLNEAKNTAKQOVATMSHLTDAQKANLTSQIE	Db 2069 QVEAAMNQVNATKAALNGTÕNLEKAKOHANTAIDĞLSHLTNAÖKEALKÖLVQQSTTVA 2126
AK	
1114 SGT	2127EAQGNEQKANNVE
Qy 106 GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDS 142	912 LQPITQPTQGILAPSV
Db 1174 GIISATNNPEMNPDTINQKASQVNSAKSALNGDEKLAAAKQTAKSDIGRLTDLNNAQRTA 1233	Db 2180 QGIIDQTTSPTLDPTV 2195
Qy 143 LIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGS 188	RESULT 37 US-09-971-536-68 : Semience 68. Application US/09971536
189 TISOAKGESNIGNKLONLNPSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFEL	; Patent No. US20020159976A1 ; GENERAL INFORMATION:

DD 576 YOLSDAGKAKLORATGNINYOLTADDLAKVMGTITITPAAVTADSNDLSFEYDGKTK 631	HERSULT 38 19.69-117-447-2 19.69-117-4
APPLICANT: Blokaberg, Leonard APPLICANT: Lubbers, Mark APPLICANT: Lubbers, Mark APPLICANT: Lubbers, Mark APPLICANT: Chisterenson, Anna APPLICANT: O'Toole, Paul APPLICANT: O'Toole, Paul APPLICANT: O'Toole, Paul APPLICANT: O'Toole, Paul APPLICANT: O'Toolear, Timothy TITLE OF INVENTION: Lactobacillus rhamnosus Polynuclectides, Polypeptides and Methode TITLE OF INVENTION: Lactobacillus rhamnosus Polynuclectides, Polypeptides and Methode TITLE OF INVENTION: Using Them FILE REPERENCE: 1045.2 CURRENT FILING DATE: 2000-106-08 PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/634,238 PRIOR APPLICATION NUMBER: U.S. No. US20020159976A1 09/724,623 PRIOR PLING DATE: 2000-11-28 PRIOR PLING DATE: 2000-11-28 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2000-108-08 PRIOR FILING DATE: 2001-08-08 PRIOR FI	09 65 TAKKSUDTVNQFISLIOTGIAISATKLEKPLQKHSTNKLAKGLDSVENIDRKLGKASNVL 124 Db 97 NSQPTYVVTYTYAGSSAKINYKQLAASYALTOTGYT. 114 Oy 125 STLASFLGTAL-AG-IELDSL-TKGDAAPDALAKASIDLINEIIGNLSGSTOT 175 1 16 IEAPSSQLAKLGSTISQ-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALDA 234 1 16 IEAPSSQLAKLGSTISQ-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALDA 234 1 16 IEAPSSQLAKLGSTISQ-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALDA 234 1 16 IEAPSSQLAKTGSTISQ-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALDA 234 1 16 IEAPSSQLAKTGSTISQ-AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALDA 234 1 176 IEAPSSQLAKTGSTISQANTKAISSTNAGLISTTAGHKSDSGVYDGK 245 Db 216 TAASQSKDLAVTUTLSDGTQKENNLYSEDFSLVEKDSANVGTYHYLLNSVGFARLQALLG 305 OY 285 SSIMLAISPLAFNNAADKFNHANALDEFAKQFRKFGYDGDHLLAEVQRGV

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535 GKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVI----QRVAETEGTDEIGLIVNAKAGN 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           651 VKRQETKVGKRIETIQYRDYELRKVGYGYGYGSTDNLKSVEEVIGSQFNDVFKGSKFNDIFH 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDG 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       788 ----SEELKTSSGS--LVGGKVT----VEKLTNNGWVD----AGTGTTVSVAPKTDA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        818 WYITSNLONYOS-NKTDHKIEQLIGKDG----SYITSDQIDKILQDKKDGTVITSQEL- 870
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----ISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAV 279
                                                                                                                                                                                                     287 TLKLQLSAAANEDTVNVNTVR-----IYKVDGNIPFALNT-----ADVSLSTDGKT 332
                                                                                                                                                                                                                                                      : |: | | : : : | | 333 ITVDAST------PFENNTEYKVVKGIKDKNGKEFKEDAFTFKLRNDAVVTQV---F 381
                                                                                                                                                                                                                                                                                                 -----VSAGVSAAAVGSAVG 365
                                                                                                                                                                                                                                                                                                                              382 GTNVTNNTSVNLAAGTFDTDDTLTVVFDKLLAPETVNSSNVTITDVETGKRIPVIASTSG 441
                                                                                                                                                                                                                                                                                                                                                             366 TPIALLV--AGVTG------LISGILEASKQAMFESVAN------RLQGKIL 403
                                                                                                                                                                                                                                                                                                                                                                                                                           E-----WEKQNGGQN-----YFDKGYDSRYA----AYLANNLKFL-----SE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                             502 STGSLITINVWGKLAGGVNEAGTYYPGLQFTTTFATKLDESTLADNFVLVEKESGTVVASE 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 LNKELEAERVIAITQ-QRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAKT-----LTAGTESRERLTN 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               591 DDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEV 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746 TEGODVTAPTVTKVFK-------GDSLKDADAV--TTLTNVDAGOKFTIOF- 787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------KASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI 165
                                                                       177 KTTRDLLRSTFKAKAQELRDSLIYDITVAMKAREVQDAVKAGNLDK---AKAAVDQINQY 233
                                                                                                          166 IGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLNFSKT-NLGLEIITGLLSG 224
                                                                                                                                                                                                                                   280 AALITSSIMLAISPLAFMNAAD-KFNHANALDEFAKQFRK----FGYDGDHLLAEYQRGV 334
                                                                                                                                                                                                                                                                                                                                                                                            442 STITITLKEALVTGKQYKLAINNVKTLTGYNAEAYELVFTANASAPTVATAPTTLGGTTL 501
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APPLICANT: Kleanthous, Harold
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miler, Charles
APPLICANT: Miler, Charles
APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REPERENCE: 06132/047002
CURRENT APPLICATION NUMBER: US/08/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 522
LENGTH: 2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1960 AGLGGIDLQNPEKLIGSMSINDLLS------KKGLFNQITGFISANDIGQVISVML 2009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1903 NSVIĠGYLTPEQKNQTLSQLLGQNNFDNLMNDSGLNTAIK--DLIROKLGF-WTGLVGGL 1959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 TKAISSYVLAQRVAAGLSTTGAVAALITSS------IMLAISPLAFMNAADKFN- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 DSLIKKGDAAPDALAKASIDLINEIIG-----NLSQSTQTIEAFSSQLAK--LGSTI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----HANALDEFAK--------QFRKFGYDGDHLLAEYQ-------- 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FONENFSKTNLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.8%; Score 175; DB 12; Length 2893; Best Local Similarity 18.2%; Pred. No. 0.0056; Matches 199; Conservative 149; Mismatches 378; Indels 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RGVGTIEASLTTISTALGAVSAGVSAAAVGSAVG-----
; Sequence 522, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
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                       2484 FTPPTLQDYIVGIQGQSALNQIEAVGGNAIKWLSTLMMETKENPFFRAPIYLKNHSLNEIL 2543
                                                                                           3544 GVTKDLQNTASLISNPNFRDNATNLLE----LASYTQQTSRLT------KLS 2585
                                                                                                                                                 2630 QGVGGASFISGGNG---TLYGLNAGYDRLVKNVILGGYVAYGYSDF-----NGNIMHS 2679
                                                                                                                                                                                                                                                                                        2680 LGNNVDVGMYARAFLKRNEFTLSANETYGGNATSINSSNSLLSVLNQRYNYNTWTTSVNG 2739
                                                                                                                                                                                                                                                                                                                                             SRXYFGKNSYYFVTARLGRDLLIKSKGSNTVR-FVGENTLLYRKGEVFNTFASVITGGEM 2858
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-----AERVIAITOORWDNNIGELAG----ITKLGERIKSGKAYADAFEDGKKVEAGS 491
                                                                                                                            NWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMN-----
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                                                               NITLDAKTGIIDISNSN--GKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVK
                                                                                                                                                                                           -----IDGGDGHDRVFYSKDGGFG----NITVDGTSATEAGSYTVNRKVARGDIYHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: PROTECTIVE RECOMBINANT HARMOPHILUS INFLUENZAE HIGH
TITLE OF INVENTION: MOLECULAR WEIGHT PROTEINS
FILE REFERENCE: 1038-1239MIS
FILE REFERENCE: 1038-1239MIS
CURRENT APPLICATION NUMBER: US/10/193, 764
PRIOR APPLICATION NUMBER: 09/167,568
PRIOR FILING DATE: 1998-10-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-193-764-63; Application US/10193764; Sequence 63, Application US/1013943A1; GENERAL INFORMATION: APPLICANT: LOOSMOTE, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Haemophilus influenzae
US-10-193-764-63
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 63
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204 TVGKDGSVN-LIGGKVKNEGVISVNGGSISLLAGQKITISDIINPTITYSIAAPENEAVN 262
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                                                                       V-VKRQETKVGKRTETIQYRDYELRKVGYGYGSTDNLKSVEEVIGSQFNDVFKGSKFNDI 708
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                                                                                                                                                                                                                                                          -----FRKGDGND 772
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                                                                                                                                                                                                                                                                                                                                                                                                                     FHSGEGDDLLDGGAGDDRLFGGKG------NDRLSGDE-----GD-DLLD
                                                   590 NDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHE
                                                                                                                                                                                                                                                                                                                            TLYDGTGN------DKLAPADANISDIMIERTKEGIIVKRNDH-SGSINIPRWYIT-
                                                                                                                                                                                                                                                            G----GSGDDVLNGG----AGNDVYI-----
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GenCore version 5.1.6 ,
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using sw model - protein search, OM protein February 17, 2004, 10:09:49; Search time 46 Seconds (without alignments) 3198.686 Million cell updates/sec Run on:

US-10-069-799-5 4647 1 MSNINVIKSNIQAGLNSTKS.....SSNALQPITQPTQGILAPSV 927 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 segs, 158726573 residues Searched:

1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 19Jun03:*

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18: /SIDS1/gcgdata/geneseqg/geneseqg-emb1/AA1999.DAT:*

19: /SIDS1/gcgdata/geneseqg/geneseqg-emb1/AA1999.DAT:*

20: /SIDS1/gcgdata/geneseqg/geneseqg-emb1/AA1999.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	M. bovis Dalton 2d	Chimeric protein #	Bovine IL-2/Pasteu	Bovine IL-2 - LKT	Leukotoxin protein	Bovine IL-2/LKT ch	Recombinant leukot	Recombinant leukot	Recombinant leukot
	Ω	AAB62110	AAW13866	AAB21073	AAR22103	AAR43865	AAR52747	AAR42385	AAR42380	AAR42378
	DB	22	18	21	13	14	15	14	14	14
	Length	927	1098	1098	1098	953	1098	924	924	924
* Query	e Match Length DB ID	100.0	50.2	50.2	50.2	50.1	50.1	50.1	50.1	50.1
	Score	4647	2334	2334	2332	2329	2327	2326.5	2326.5	2326.5
Result	No.	г	7	3	4	ß	9	7	80	6

LKT352. Pasteurel Leukotoxin 352 pro	Recombinant leukot		LKT-GnRH protein f	LKT-GnRH chimeric	Bovine IFNgamma/LK	Chimeric protein #	Bovine gamma-IFN/P	105kD PTX protein	PtxA protein of Pa	Pasteurella haemol	Somatostatin-leuko	GnRH-leukotoxin ge	Leukotoxin 352 enc	P. haemolytica tru	Leukotoxin from P.	Rotavirus VP4-leuk	P. suis leukotoxin	APPA haemolysin an	ApxIIC protein. A	A. pleuropneumonia	ApxIIIB protein.	A. pleuropneumonia	Leukotoxin AppIIIA	ApxIA protein. Ac	 A. pleuropneumonia 	LhaA (low homology	Pasteurella haemol	Enterohaemorrhagic	Pasteurella haemol	LKT-GnRH chimeric	LKT-GnRH chimeric	Leukotoxin/gonadot	Gonadotropin relea	Leukotoxin carrier
AAR14482 AAR34545	AAR50291	AAW7956	AAW0394	AAW7956		AAW13867	•	AAR07167	AAR60072	AAE04638		AAR34547			AAR15159			•	•	•	•		_						·			AAY5836		AAY33929
	15																															21		
926	926	926	776	977	1069	1069	1069	953	953	953	943	936	924	926	953	951	934	926	926	926	1049	1049	1244	1022	1022	1023	608	758	450	544	695	695	9	490
50.1	50.1	50.1	50.1	50.1	50.1	50.1	50.1	٠.	0.09	0.09	90.09	6.61	6.61	6.6	8.61	49.8	49.4	48.1	48.1	48.1	41.4	41.4	41.4	97.9		37.2	31.5	9.62	25.0	19.5	19.4	19.4	19.4	19.3
10.10		5,					٠,																			•								
2326.5	2326.5					2326.5	2326.5	2325	2325	2325	2323.5	2318.5	2317.5	2317.5	2313	2312.5	2297.	2236.5	2236.5	2236.5	1924	1924	1924	1763.5	1763.5	1727	1464.	1376.5	1159.5	0	90	901	90	897.5
10	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAB62110 standard; Protein; 927 AA AAB62110; RESULT 1 AAB62110

M. bovis Dalton 2d RTX toxin A subunit.

(first entry)

29-MAY-2001

Moraxella, antigen; immune response; infection; RTX toxin; vaccine; antibacterial; A subunit.

Moraxella bovis.

WO200116172-A1.

08-MAR-2001

31-AUG-2000; 2000WO-AU01048.

99AU-0002571. 31-AUG-1999; (CSIR) COMMONWEALTH SCI & IND RES ORG. (UYME) UNIV MELBOURNE.

Tennent J; Farn J, Strugnell R,

WPI; 2001-235092/24. N-PSDB; AAF57290 Novel Moraxella bovis antigen useful in compositions for raising immune

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AAW13866
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                                                                                                                                                                                                                                                                                                                                           SNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFS 180
                                                                                                                                                                                                                                                                                                                                                                                                   SNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQLAKLGSTISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVAAGFELSNOVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFNHANALDEFAKÇFRKFGYDGDHLLAEYQRGVGTIEASLITISTALGAVSAGVSAAAV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSAVGIPIALLVAGVIGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYD 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780
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                                                       The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polynucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRYAAYLANNIKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADA
                                                                                                                                                                                                                                                                1 MSNINVIKSNIQAGINSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
                                                                                                                                                                                                                                                                                MSNINVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                             SQLAKLGSTISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 NKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTETIQYRDYELRKVGYGYGYGTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNFVYIFRKGDGNDTLYDGTGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYI SNLQNYQSNKTDHKIEQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGK
                                                                                                                                                                                                                                    Gaps
has protease, lipase or hemolysin activity
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                     Length 927;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                     100.0%; Score 4647; DB 22;
100.0%; Pred. No. 4.1e-281;
ive 0; Mismatches 0;
                             Fig 5; 60pp; English
                                                                                                                                                                                                                     Local Similarity 100.
Les 927; Conservative
 animal,
                                                                                                                                                                           927 AA;
                             56;
 response
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                             Claim
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13;
                             900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukotoxin is a truncated leukotoxin lacking leukotoxic activity, especially LKT352. The chimeric proteins can be used for the production if vaccines against respiratory diseases such as pneumonia, particularly fibrinous pneumonia caused by P. Daemolytica, including shipping fever in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTX cytotoxin; cytokine; immunogen; chimeric protein; cytokine; vaccine; interleukin-2; IL-2; gamma interferon; gamma IFN; leukotoxin; pneumonia; Pasteurella haemolytica; LKT352; respiratory disease; shipping fever; fibrinous pneumonia; cattle; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW13866 and AAW13867 represent immunogenic chimeric proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ilarity 50.1%; Pred. No. 7.4e-137;
Conservative 175; Mismatches 263;
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                                                                                                                                                                                                                                                                                    Protein; 1098
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UNIV SASKATCHEWAN.
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91US-0777715.
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(first entry)
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N-PSDB; AAT60032.
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                                                                                                                                                                                                                                                                               standard;
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22-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-1991;
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12-MAY-1997
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  841
                                                   841
                                                                                                   901
                                                                                                                                                      901
                                                                                                                                                                                                                                                                                                                                  AAW13866;
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Best Local 8
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                                                                                                                                                                                                                                                                                                                     TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD 833
                                                  126 TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK 185
                                                                347
                                                                                    484
                                                                                                                                                                                                            647
                                                                                                                                                                                                                          KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK 544
                                                                                                                                                                                                                                 545 FGRVKNWQVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQ 597
                                                                                                                                                                                                                                                                               GKWNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
                                                                                                                                                                                                                                                                                                                                         LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG 777
                                                                                                                                                                                                                                                                                                                                                       IDGNDGNDRLFGGKGDDILDGGNGDDFIDGGKGNDLLHGGKGDDIFVHRKGDGNDIITDS 945
                                                                                                                                                                                                                                                                                                                                                                                                 HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
                      AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125
                                                                                                          304
                                                                                                                                     HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
        231
                                                                                                                                                                 GTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA 424
                                                          GTTEIDGGGGYDRVHYSR-GNYGALTIDATKETEGGSYTVNRFVETGKALHEVTSTHTAL
                                                                                                                                                                                                      LGSTISQAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA
                                                                                                          GFELSNOVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN
                                                                                                                                                                                              AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
                                                                                                                                                                                                                                                                                                              VGKRTETIQYRDYBLRKVGYGYGYGYDILKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
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Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein.

19-DEC-2000

AAB21073;

AAB21073 ID AAB3 XX AC AAB3 XX DT 19-1 XX DE BOV3

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AAB21073 standard; Protein; 1098

RESULT

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immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN) or an active fragment thereof, linked to an epitope of a Pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting respiratory disease associated with Pasteurella species, affecting exposed cattle and resulting in a 2-5% mortality rate in the exposed cattle and resulting in a 2-5% mortality rate in the specied population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever pneumonia, in livestock. The present sequence represents a fusion protein comprising bovine interleukin-2 (IL-2) and pasteurella haemolytica leukotoxin, which may also be used as an anti-Pasteurella vaccine.
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Bovine IL-2; interleukin-2; leukotoxin; LKT; respiratory disease; pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLOKHSTNKLAKGLDSVENIDRKLGKASNVLS
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50.1%; Pred. No. 7.4e-137;
ive 175; Mismatches 263;
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96US-0681479.
90US-0571301.
91US-0777715.
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Pasteurena
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Interleukin 2; leuko-toxin; vaccine; pneumonia; respiratory Z - LKT fusion protein. AAR22103 standard; Protein; 1098 91WO-CA00299 90US-0571301 (first entry) Pasteurella haemolytica Ä (POTT/) POTTER 22-AUG-1991; 22-AUG-1990; 06-JUL-1992 Bovine IL-2 WO9203558-A 05-MAR-1992 Bos taurus. diseases. AAR22103

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545 FGRVKNWQVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQ 597

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GTTEIDGGGGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTAL 826

GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK

Hughes HPA; Сащров М, WPI; 1992-096901/12 N-PSDB; AAQ22771 Ą, Potter

encodes fusion protein as vaccine for animal pneumonia Interleukin 2-leuko-toxin gene fusion useful

Claim 20; Fig 3; 68pp; English

The IL-2-LKT protein was encoded by a chimeric gene contg. the bovine IL-2 gene fused to the DNA encoding at least one epitope of leukorcoxin from P. haemolytica. IL-2-LKT was gel purified and ligated into the expression vector pdf433 lac1. The resulting clone pAA356 (ATCC 68386) contd. the desired gene fusion under the control of the E. coli lac promoter. The protein produced by the acceptable vehicle, e.g. a carrier homologous to, a rotaxirus VP6 inner capsid protein. The vaccine can be used for preventing or ameliorating respiratory diseases in animals e.g. shipping fever pneumonia

1098 AA; Sequence

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See also AAR24124,5.

13; 364 647 544 125 GIOSILGSVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQ 347 244 527 484 126 TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK 185 GPELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304 GTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA 424 KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK |: |: |: || : || : || :| || || || AQTSLGTIQTAIGLTERGIVLSAPQIDKLLQK---TRAGQALGSAESIVQNANRAKTVLS AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA HANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET 26; Length 1098; Indels 50.2%; Score 2332; DB 13; larity 50.1%; Pred. No. 9.9e-137; Conservative 174; Mismatches 264; Query Match Best Local Similarity Matches 465; Conserv 173 99 186 245 408 305 468 365 425 588 485

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                                     LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG
                                                                                                               HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
                                                                                                                                                                                                                                                                                                           determinants; peptides; vaccine; supernatant; leukotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One or more biologically pure antigenic determinants of the leukotoxin protein comprising of at least six amino acids is a component of a new vaccine for animals. The vaccine alicits an enhanced immune response after challenge with Pasteurella haemolytica. The vaccines other component is a bacterial free culture supernatant derived from a culture of Pasteurella free the contraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine for preventing Pasteurella haemolytica infections contains leukotoxin protein antigenic determinants and P. haemolytica culture supernatant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.1%; Score 2329; DB 14; Length Sest Local Similarity 49.9%; Pred. No. 1.3e-136; Matches 464; Conservative 175; Mismatches 264; Indels
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(first entry)
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22-DEC-1993
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                                                                                                                       383 ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKONHGKOYFENGYDARYL
                                                                                                                                                                                                                                                                                                                                                                                                                  LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
28 QSLTQAG-SSLKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAAEBLGIEVQREERNNIAT
                                                             186 LGSTISQAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA
                                                                                                                                                                                203 FGSKLQNIKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGA
                                                                                                                                                                                                                        245 GFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN
                                                                                                                                                                                                                                                                                                                                             365 GTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA
                                                                                                                                                                                                                                                                                                                                                                                                    425 AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGRVKNWQVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 VCKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
                                               AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |:: | :: | : | : | : | : | : | ISSVSAFTSSNDSRNVLVAPTSMLDQSL
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(first entry)
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946 DGNDKLSFSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-D 1003
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                                                                                                                                                      834 HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK 893
                                                                                                                                                                                                 GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK 657
                                                                                                                                                                                                                                                                                                                      LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG 777
                                                                         KKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK
                                                                                         TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
              AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG
                                                                                                                                                                                                                                                             VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant leukotoxin peptide from plasmid pCRR28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVGSMALFGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pontarollo RA,
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920S-0893426.
93US-0038287.
93US-0038288.
93US-0038719.
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29-MAR-1993;
29-MAR-1993;
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19-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPIALLVAGVTGLISGILEASKQAMPESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a fusion between bovine interleukin-2 (IL2) and Pasteurella haemolytica leukotoxin (ITK). The leukotoxin gene, ItkA, was isolated from a gene library of P. haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also be used to raise mono-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic fusion proteins of gamma-interferon and immunogenic
leukotoxin - used in vaccines and to raise monoclonal and polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.1%; Score 2327; DB 15; Length 1098; Best Local Similarity 49.9%; Pred. No. 2e-136; Matches 464; Conservative 175; Mismatches 264; Indels 26;
                            Bovine, interleukin-2, IL2, P. haemolytica, leukotoxin, LTK;
ltkA, chromosome walking, fusion protein, vaccine,
monoclonal, polyclonal, antibody, ss.
Bovine IL-2/LKT chimeric protein encoded by plasmid pAA356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and polyclonal antibodies. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                         Pasteurella heamolytica - chimera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 3; 56pp; English.
                                                                                                                                                                                                                                                                                                                        Potter
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                                                                                                                                                                                                   91US-0777715
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                                                                                                           Bos taurus - chimera
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                                                                                                                                                                                                   16-OCT-1991;
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                                                                                                           GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                  781 FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                                          785 FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLONYQSNKTDHKIEQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus somnus immunogenic proteins used in vaccines -
selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                   Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
thromboembolic meningoencephalitis; septicaemia; arthritis;
pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                           Recombinant leukotoxin peptide (split) from plasmid pGCH4
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                                                                                                                                                   901 FGTANSVSSNALQPITQPTQGI 922
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                                                                                                                                                                            FTSSNDSRNVLVAPTSMLDOSL
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92US-0893424.
92US-0893426.
93US-0038287.
93US-0038288.
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19-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                            TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPIALL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS 491
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                                                                                                                        The lppB gene protein was expressed in E. coli as a fusion to the Pasteurella haemolytica leukotoxin gene lkth coded for by plasmid pAA512. The llpB gene fragment was taken from pMS11. LppB can be used in vaccines for preventing or treating H. somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in vertebrates.
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                                           lus somnus immunogenic proteins used in vaccines -
from haemin-binding protein, haemolysin, LppB and LppC,
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11 Similarity 50.0%; Pred. No. 1.7e-136;
461; Conservative 174; Mismatches 262;
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                                                                                                Disclosure; Fig 11; 119pp; English
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                                             Haemophilus somnus
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                                                                                                                                                 VIGNVTKAISSYVLAORVAAGLSTIGAVAALITSSIMLAISPLAFMNAADKFNHANALDE 311
                                                                                                                                                                              FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL 371
                                                                                                                                                                                                          VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
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                              INSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADBLGIARLAEEPNHTETAKKSVDT
                Gaps
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               25;
 14; Length
cch 50.1%; Score 2326.5; DB 14; Lengtlas Similarity 50.0%; Pred. No. 1.7e-136; 461; Conservative 174; Mismatches 262; Indels
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standard; Protein; 924 AA

AAR42378

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                                                                                                    Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
thromboembolic meningoencephalitis; septicaemia; arthritis;
pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and and corresp. DNA
                                                             Recombinant leukotoxin peptide (split) from plasmid pGCH5
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92US-0893424.
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(updated)
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The LKT352 gene was prepd. as follows: lkth, an Mael fragment contg. the gene was prepd. as follows: lkth, an Mael fragment contg. the gene was ligated into the Smal site of pUC13 to form pAA19. From this, two constructs were made in the ptac-based vector, pGH432:lac1 digested with Smal. One, pAA342, consisted of the 5' Ahalli fragment from lkth while the other, pAA345, contained the entire Mael fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed full cleukotoxin at very low levels. The 3' end of the lkth gene of pAA345 was therefore ligated to Styl/Bamil digested hAA342 to yield pAA352 contg. the LKT32 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with cother P heemolylytica antigens, e.g. finbrial protein, plasmin creeptor or 50% outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                                                                                 Vaccines for Pasteurella haemolytica infection in cattle -
comprise sub-unit antigens from P haemolytica fimbrial protein,
plasmin receptor, 50 K outer membrane protein and leukotoxin.
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Best Local Similarity 50.0%; Pred. No. 1.7e-136;
Matches 461; Conservative 174; Mismatches 262; Indels
Lawman MJP;
Potter AA,
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Barink
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                                                                                                                                                                                                                                                                                                                                                                       GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
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                                                                                GEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEK 661
                                                                                                                                                                                                        DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA 784
543 KITDGAASSTFDLTNVVQRIGIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDG 602
                                                                                                                           IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
                                                                                                                                                Gene libraries of P. haemolytica Al (strain B122) were constructed in lambda gtll and pUCl3. Resulting clones were used to transform E. coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vector, LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGTANSVSSNALQPITQPTQGI 922
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FTSSNDSRNVLVAPTSMLDQSL 917
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23-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 PAKOFRKFGYDGDHLLAEYORGVGTIEASLITISTALGAVSAGVSAAAVGSAVGTPIALL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 YAERFKKIGYDGDNLLAEYQRGTGTIDASVTAINTALAAIAGGVSAAAAGSVIASPIALL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGNVTKAISSYVLAQRVAAGLSTIGAVAALIISSIMLAISPLAFMNAADKFNHANALDE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAGVTGLISGILEASKQAMFESVANRLOGKILEWEKONGGONYFDKGYDSRYAAYLANNL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                   fragment was obtd. Progressively larger clones were isolated by chromosome walking to isolate full length recombinants of ca. 8kb, chromosome walking to isolate full length recombinants of ca. 8kb, in pAALI4. The clone was subjected to restriction enzyme dispestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing truncated leukotoxin at low levels. The 3' end of the lkth gene from the full length clone was ligated to the truncated gene clone to yield plasmid pAA352. The clone was used to produce chimeric proteins by gene fusion with an intigen coding sequence, e.g. the coding sequence of somatostatin, gonadotrophin releasing hormone or rotavirus viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger amtigen acarrier protein to.bring about a larger commune response than the antigen alone. Immunisation with these antigened on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 50.1%; Score 2326.5; DB 14; Length 926; Local Similarity 50.0%; Pred. No. 1.7e-136; es 461; Conservative 174; Mismatches 262; Indels 25;
colonies were screened for their ability to produce leukotoxin incubating cell lysates with bovine neutrophils and measuring trelease of lactate dehydrogenase from the neutrophils. A 4kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              926 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAW79568
ID AAW7
                                                     840
                                                                                                                       FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                                                       GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A vaccine comprising an outer membrane protein (OMP) extract of Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic Pasteurella haemolytica leukotoxin homologous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352.

Two expression constructs were made. One, pAA352, contained the S4. Ahall fragment of the lkA gene, while the other, pAA345, contained the entire lktA gene. pAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full length leukotoxin at very low levels. Therefore, the 3' end of the lktA gene was ligated into pAA342, yielding plasmid pAA352. LKT352 or new leukotoxin is 98% homologous to authentic
                                                                                                                                                                                                                                                                                                                                                                         'accine, outer membrane protein; OMP; Haemophilus somnus; .ron regulated protein; leukotoxin; Pasteurella haemolytica;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NB: the protein sequence in Fig 5 comprises 926 amino acids,
however this protein is described in the text as having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus somnus outer membrane protein extract
enriched with iron-regulated proteins, opt. contg.
leuco:toxin antigens, for use as vaccine
                                                                                                                                                                                                                                                                                                                                               Recombinant leukotoxin from plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica Al (strain B122)
                                                                                                                                                                                          FTSSNDSRNVLVAPTSMLDQSL 917
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                                                                                                                                                                FGTANSVSSNALQPITQPTQGI
                                                                                                                                                                                                                                                               standard; Protein; 926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0908253
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-092909/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              931 amino acids.
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                                                                                                                          133 TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ 192
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                                                                                              IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
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                                        LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                    AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO
                                                                                                                                                                                                                                                  PAKOFRKFGYDGDHILAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL
                                                                                                                                                                                                                                                                                          VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL
                                                                                                                                                                                                                                                                                                                                                                            492 NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
                     25;
Length 926;
                     Indels
 Query Match 50.1%; Score 2326.5; DB 15. Best Local Similarity 50.0%; Pred. No. 1.7e-136; Matches 461; Conservative 174; Mismatches 262;
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AAW79568 standard; Protein; 926

RESULT 13

422 491 482 551 542 604 602 664 661 724 720 784 780 840 838

371 362

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GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
243 VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES 302
                                                                                                                                                                                       GQNGERITSKQVDDLI--AKGNGKITQDELSKVVDNYELLKHS-KNVTNSLDKLISSVSA
                                                                                   VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukotoxin, LKT, gonadotropin-releasing hormone, GnRH;
fusion protein; immunogen; vaccine; fertility control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain B122;
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/label= GnRH_repeat_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGTANSVSSNALQPITQPTQGI 922
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/label= LKT
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                                                                                                                                                                                    Gonadotropin releasing hormone, GnHR, chimera, leukotoxin polypeptide,
multimer, vaccine, tumour, Leukotoxin 352, LKT 352, lktA, plasmid pAA352,
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                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
11..924
/note= "Recombinant leukotoxin peptide"
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                                                                                                                                      Leukotoxin 352 polypeptide
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The present sequence represents the LKT-GARH chimeric protein from pCB113. This plasmid contains the LKT 352 polypeptide (AAM79568) fused to four copies of the GARH peptide. This chimera lacks cytotoxic activity which enables there to be an increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated LKT to be expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukotoxin polypeptide, several multimers, and a GARH
                                                                                                               GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL 900
                                                                                                                                                                                                                                                                                     Chimera, pCB113; LKT 352; GnRH; Gonadotropin releasing hormone, multimer; cytotoxic activity; antigen presentation; immune response; vaccine;
DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY I FRKGDGNDTLYDGTGNDKLA
                                                                                                                                                                      GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
                                                                                              IQYRDYELRKVGYGYQYDDILKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
                                                                                                                                                                                                            PADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                                                                                                                                                                              Chimeric protein of leukotoxin and gonadotropin releasing hormone - useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Figure 5.1-8; 118pp; English.
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N-PSDB; AAV61531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NITLDAKTGIIDISNSNGKKTQALHFISPLLIAGTESRERLINGKYSYINKLKFGRVKNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
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                                                                                                                                                                                                                                                      A chimeric protein (AAW03942) is composed of a fusion between a truncated leukotoxin (LKT-352) from Pasteurella haemolytica (see also AAW03945) and a 4-copy gonadoliberin-releasing hormone (GnRH) repeat sequence (see also AAW03944). It is the product of a chimeric gene (AAT37176) produced by ligating a synthetic sequence for the 4-copy GnRH into vector pAAJ52 (ATCC 68283), which carries the LKT-352 gene. Recombinant plasmid pCBL13 (LKT 352:4 copy GnRH, ATCC 69749) was obtd. Escherichia coli transformants produced the chimeric protein, which is useful as a vaccine for fertility control, esp. immunological sterilisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.1%; Score 2326.5; DB 17; Length 977; 50.0%; Pred. No. 1.9e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                      Gonadotropin-releasing hormone multimer fusion proteins - with leukotoxin polypeptide for increased immunogenicity, useful in antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 174; Mismatches 262; Indels
                                                                                                                                                                                                                              Claim 7; Fig 5A-5H; 87pp; English.
                 96WO-CA00049
                                           95US-0387156
                                                                        SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                       domestic or farm animals
                                                                                                   Potter AA;
                                                                                                                              WPI; 1996-384447/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                977 AA
                                                                                                                                           N-PSDB; AAT37176
                                                                     UYSA-) UNIV
                 24-JAN-1996;
                                            10-FEB-1995;
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16-OCT-1991;
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                                                                 25-MAR-2003
01-JUL-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                        604
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                                                                                                                                                                                                                                                                                                                                                                       661
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                                                                                                        99
sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
                                                                                                                                                                            SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN
                                                                                                                                                                                                                  363 VSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKONHGKONYFENGYDARYLANLQDNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQYRDYELRKVGYGYGYGYDDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
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                                                                                     15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                       7 LSFPKTGAKKIILYIPONYOYDTEOGNGLODLVKAAEELGIEVOREERNNIATAQTSLGT
                                                                                                                           73 VNOFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSPLG
                                                                                                                                                                                                      AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNO
                                                                                                                                                                                                                                                                                  312 PAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL
                                                                                                                                                                                                                                                                                                                       VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL
                                                                                                                                                                                                                                                                                                                                                                                                  492 NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
                                                                                                                                                                                                                                                                                                                                                                                                             : [|: ||||:||| ||| :| :|| ||| ||| ||| :|| 100LDSANGIIDVSNGKAKTQHIFRTPLLITPGTEHRERVQTGKYEYITKLNINRVDSW
                                                                                                                                                                                                                                                                                                                                                                                                                                         552 QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                   Gaps
                                                                  25;
                                                                 Matches 461; Conservative 174; Mismatches 262; Indels
                                               Score 2326.5; DB 19;
Pred. No. 1.9e-136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGTANSVSSNALQPITQPTQGI 922
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                                                50.1%;
                                                         Similarity
                            977 AA;
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                                                                                                                                                                                                                                               e; interleukin-2; IL2; P. haemolytica; leukotoxin; LTK; IFN; chromosome walking; fusion protein; vaccine; interferon; gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic fusion proteins of gamma-interferon and immunogenic
leukotoxin - used in vaccines and to raise monoclonal and polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a fusion between bovine gamma interferon (IFNgamma) and Pasteurella haemolytica leukotoxin (LTK). The leukotoxin gene, ltkA, was isolated from a gene library of P. haemolytica by chromosome walking. Immunogenic fusion proteins such as this can be used in vaccine compositions. It can also be used to raise mono- and polyclonal antibodies. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Recombinant leukotoxin peptide [split]"
                                                                                                                                                                                             Bovine IFNgamma/LKT chimeric protein encoded by plasmid pAA497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 50.1%; Score 2326.5; DB 15; Best Local Similarity 50.0%; Pred. No. 2.1e-136; Matches 461; Conservative 174; Mismatches 262; Ii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927..1069
/note= "Bovine IFNgamma"
standard; Protein; 1069 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 Pasteurella heamolytica - chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potter A;
                                                                                                                                                                                                                                                                                                             monoclonal; polyclonal; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 7; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CIBA GEIGY CANADA LTD
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                                                                                                               (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campos M, Hughes HPA,
                                                                                                                                                                                                                                                                                                                                                                                                 - chimera
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20-DEC-1993;
22-AUG-1990;
16-OCT-1991;
                                                                          20-DEC-1993;
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                        14-JAN-1997
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                        AKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
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toxin - useful in vaccines, esp. against
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N-PSDB; AAT60033.
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Best Local Similarity
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                                                                             GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET 664
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pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
                         QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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N-PSDB; AAA72484.
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                                                                                                                                                                  also
                                                                                fusion protein is immunogenic, and may be used in a natitier pasteurella vaccine composition. Pasteurella species, especially pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting 15-30% of exposed cattle and resulting in a 2-5% mortality are in the exposed population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever pneumonia, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
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                                        this sequence a fusion protein comprising bovine gamma-interferon (gamma-IFN) and Pasteurella haemolytica leukotoxin (LKT). The
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Claim 8; Column 45-50; 56pp; English
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                                                                                                                            HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
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                                                                                                                                               443 ANLQDNMKFLININKELQAERVIAITQQQWDNNIGDLAGISRLGEKVLSGKAYVDAFEEG
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                                                      GFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN
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   FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene product is antigenic to P.haemolytica, and may be used as vaccine for immunisation against shipping fever. Abs raised to antigen may be used in passive immunisation and diagnosis.
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5 kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine against shipping fever in cattle - contains pasteurella haemolytica antigen of molecular wt. 105
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FTSSNDSRNVLVAPTSMLDQSL 917
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N-PSDB; AAQ06074.
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Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
                                                                                                                                                                                                                         LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG
                                                                                                                                                        778 TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTD
             GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
                                                                          VCKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                                                                                                  834 HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is Pasteurella (Mannheimia) haemolytica full length leukotoxin protein. The present invention relates to modified leukotoxin DNA sequences, wherein the modification comprises the
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/label= Hydrophobic_transmembrane_domain_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukotoxin; respiratory disease; infection; therapy; i
antibacterial; vaccine; transgenic plant; animal feed.
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                                                                                                                                                                                                                                                                                                                                 LVGSMALFGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                                                                   | | : | : | : | : | : | : | : | | : | ISSVSAFTSSNDSRNVLVAAPTSMLDQSL 944
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                                                                                                                                                                                                                                                                                                                This protein is a 105 kD antigen which may be used in vaccines to protect cattle against shipping fever. The antigen is also useful for raising antisera which can be used for passive immunisation (for treatment or temporary prophylaxis) and also to raise antibodies which can be used in immunoassay methods for the detection of Pasteurella haemolytica antigens in biological fluids. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 953;
                                                                                                                                                                                                                    New purified antigen from Pasteurella haemolytica - useful i
vaccines against shipping fever of cattle, also for raising
antibodies useful in diagnosis and passive immunisation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 2125; DB 15; Best Local Similarity 49.9%; Pred. No. 2.2e-136; Matches 464; Conservative 175; Mismatches 264;
                                                                                                                                           Engler M, Highlander S, Weinstock G;
                                                                                                                                                                                                                                                                                    Disclosure; Figure 9; 35pp; English.
                            86US-0935806.
87US-0085430.
90US-0540261.
92US-0899100
                                                                            92US-0899100
                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                        WPI; 1994-255245/31.
N-PSDB; AAQ70050.
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                             28-NOV-1986;
13-AUG-1987;
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15-JUN-1992;
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                                                                                                                                                                                                                                                                     OSLTQAG-SSLKTGAKKIILYIPQNYQYDTEQGNGLQDLVKAAEELGIEVQREERNNIAT 86
removal of DNA sequence encoding the amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a ruminant, to prevent or treat respiratory diseases.
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                                                                                                                                                                          Length 953;
                                                                                                                                                                          50.0%; Score 2325; DB 22; Length ilarity 49.9%; Pred. No. 2.2e-136; Conservative 175; Mismatches 264; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
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/note= "recombinant leukotoxin protein"
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                                                             LVGSMALFGTANSVSSNALQPITQPTQGI 922
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                                                                                                |: |:: | : : | : | : | LISSVSAFTSSNDSRNVLVAPTSMLDQSL
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(first entry)
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(Updated on 25-MAR
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23-AUG-1993
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GnRH-leukotoxin gene fusion prod
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14-OCT-1992;
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SVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQFGSKLQN 182
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                                            NITLDAKTGIIDISNSNGKKTQALHFISPLLIAGTESRERLINGKYSYINKLKFGRVKNW
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          AKGFSN1GNKLONL-NFSKTNLGLE11TGLLSG1SAGFALADKNASTGKKVAAGFELSNQ
                                                                                                                                                                              FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPIALL
                                                                                                                                                                                                                                                    KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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AAR34547 standard; Protein; 936

RESULT 23

(updated)
(first entry)

AAR34547; 25-MAR-2003 23-AUG-1993

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Vector; LKT 352; flanking; recombinant; antigen; somatostat gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.9%; Score 2318.5; DB 14; Lengt llarity 49.9%; Pred. No. 5.6e-136; Conservative 174; Mismatches 263; Indels
                                                                                                                                                                                       ...........recombinant leukotoxin protein"
/note= "recombinant leukotoxin protein"
927..936
/note= "GnRH"
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                                                                                                                                                      Location/Qualifiers
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                                                                            KFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS 491
                                                                                                         PAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPIALL
                                                                                                  NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKOW
                                                                                                                          QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                 GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
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                                                                                                                                                                                                                        FADANI SDIMI ERTKEGI I VKRNDHSGSINI PRWY - - - - ITSNLQNYQSNKTDHKI EQLI
                                                                                                                                                                                                                                respiratory disease; shipping fever pneumonia
                                                                                                                                                                                                                                                                                                                                                    Leukotoxin 352 encoded by plasmid pAA352
                                                                                                                                                                                                                                                                                                                                                                           Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                              | ::| : | :
FTSSNDSRNVLVAPTSMLDQSL 917
                                                                                                                                                                                                                                                                       FGTANSVSSNALQPITQPTQGI 922
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                                                                                                                                                                                                                                                                                                                AAR10889 standard; Protein; 924
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                                                                                                                                                                                                                                                                                                                                                               LKT; vaccine; antigen;
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IQYRDYELRKVGYGYGYGYTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KFLSELNKELEAERVIAITOORWDNNIGELAGITKIGERIKSGKAYADAFEDGKKVEAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPIALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 INSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                                                                                                                                                  Plasmid pAA352 is derived from pAA114, a clone isolated from a genomic library of P. haemolytica. The protein, designated "new leukotoxin" or "LKT 352" is 984 homologous to authentic leukotoxin. LKT 352 and pref. antigenic fragments of it, can be used in vaccines to protect cattle from respiratory diseases. They can also be used to produce antibodies for immnosfifnity purificn. of further proteins. [Fig. contg. sequence v. poor]. see also AAR10890, AAR10909, AAR10910 and AAQ10783.
                                                                                    Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases e.g. pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.9%; Score 2317.5; DB 12; Length 924; llarity 50.0%; Pred. No. 6.3e-136; Conservative 174; Mismatches 260; Indels 27;
Lawman MJP;
    Potter AA,
                                                                                                                                                                                                  Claim 13; Fig 5; 87pp; English.
  Babiuk LA,
                                             1991-000097/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 461; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              924 AA;
                                                                  N-PSDB; AAQ10272
  SD,
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243 VVGNITKAVSSYILAQRVAAGLSSTGPVAALIASTVSLAISPLAFAGIADKFNHAKSLES 302
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                                                                                                                                                                                                                                                                                             GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                         TALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ
                                                                                                                                                                                                                                           VAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNL
                                                                                                                                                                                                                                                                                                                               KFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGS
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                        VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
                                                                                                                             193 AKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQ
                                                                                                                                                                                                                              FAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALL
                                                                                                                                                                                                                                                                                                                                                                                 492 NITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
                                                                                                                                                                                                                                                                                                                                                                                                                                 QVTDGEASSKLDFSKVIQRV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGTANSVSSNALQPITQPTQGI 922
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                                                                                                                               GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                                                                                                                             IEYR-HSNNQHHAGYYTKDTLKAVEEIIGTSHNDIFKGSKFNDAFNGGDGVDTIDGNDGN
                           DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLA
                                           FADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLI
                                                                                             15 INSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A truncated leukotoxin (AAW03945), LKT 352, lacks the cytotoxic portion of the native protein from Pasteurella haemolytica. It is the product of plasmid pAA352 which carries a truncated lktA gene (AAT37179). A fusion protein (AAW03942) between LKT352 and a gonadotropin releasing hormone tetramer can be expressed in Escherichia coli. This is useful as a vaccine for fertility control, partic. immunological sterilisation of domestic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 49.9%; Score 2317.5; DB 17; Length 926; Best Local Similarity 49.8%; Pred. No. 6.3e-136; Matches 459; Conservative 175; Mismatches 263; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gonadotropin-releasing hormone multimer fusion proteins - with leukotoxin polypeptide for increased immunogenicity, useful in antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                     Leukotoxin, LKT; gonadotropin-releasing hormone, GnRH; fusion protein; immunogen; vaccine; fertility control; contraceptive; sterilisation; plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. haemolytica truncated leukotoxin (LKT352)
                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella haemolytica Al strain B122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3A-3I; 87pp; English.
                                                                                                                                                                                                 | ::| : | : | : | ETSSNDSRNVLVAPTSMLDQSL 915
                                                                                                                                                                                FGTANSVSSNALQPITQPTQGI 922
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N-PSDB; AAT37179.
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                                                                                                                     GMMIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
                                                                                                                                                  VGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
                                                                                                                                                                                                                                                                                                                         LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDG
                                                                                                                                                                                                                                                                                                                                                                                                                             TGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLONYOSNKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:toxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "recombinant leukotoxin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGSMALFGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: |:: | :: | : | : | ELISSVSAFTSSNDSRNVLVAPTSMLDOSL 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rotavirus VP4-leukotoxin gene fusion prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Rotavirus VP-4"
                       FGRVKNWQVTDGEASSKLDFSKVIQRV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF2 (AAR14223) codes for a 19.820 D protein of 166 amino acids; ORF1 codes for leukotoxin, a 101.883 D protein of 952 amino acids, which is produced on expression of pLKT5 in a host organism. The leukotoxin has cytotoxic activity specific against leukocytes. The protein is used to prepare vaccines or to raise antibodies against P. haemolytica to protect cattle from pneumonic pasteurellosis.
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Leukotoxin; probe; pasteurellosis; cytotoxicity; leukocytes.
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al Similarity 49.6%; Pred. No. 1.3e-135;
461; Conservative 176; Mismatches 266;
                                                    Pasteurella haemolytica Al (ATCC 43270)
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                                               781 FSDSNLKDLTFEKVKHNLVI-TNSKKEKVTIQNWFREADFAKEVPNYKATK-DEKIEEII
                                                                                                                                                                                                                                                                                                                  Leukotoxin, pslktC; pslktA; pslktB; calcium dependent; RTX;
cytotoxic protein; repeat of toxin; BL-3 cell; pig; lymphocyte;
immunogen; vaccine; immunisation; diarrhoea; reagent;
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/note= "glycine rich repeat sequence"
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    P. suis leukotoxin gene pslktA, protein product.

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e= "glycine rich repeat
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FTSSNDSRNVLVAPTSMLDQSL 917
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94US-0215805.
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N-PSDB; AAT45417.
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05-FEB-1997
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                         protein 4 (VP-4) gene were constructed on a Pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella theamolytica leuko.coxin gene) which had been digested with BamHI. The ligated DNA was used to transform E. coli strain MH3000. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA501. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 IQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLSGIQSILG
                                                                                                                                                                                                                                                                                                                                                                                                                                            183 IKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGAGFELANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 LNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDT
                                                                                                                                                                                                                                                                                                                              VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OVTDGEASSKLDFSKVIORV-----AETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDG
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                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                  DB 14; Length 951;
                                                                                                                                                                                                                                            Best Local Similarity 49.8%; Pred. No. 1.3e-135;
Matches 459; Conservative 174; Mismatches 264; Indels
                                                                                                                                                                                                                                 49.8%; Score 2312.5; DB 1
49.8%; Pred. No. 1.3e-135;
                                                                                                                                                                                 (Updated on 25-MAR-2003 to correct PN field.)
                2; Fig 8; 95pp; English.
                                                                                                                                                                                                          951 AA;
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porcine pleuro-pneumonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             956 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR12127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ11873.
                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1990;
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26-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                            107 LDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEII 166
                                                                                                                                                                                                                                                                                                                                                                                                        PGSSENVAKNLGNAQTLLSGIQSILGSVAAGADLDEILKNKGSELD-LAKAGLELTNSLI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                        GNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLLSGI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                     285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKQNGGQNYPDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGIT 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAG 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSNINV-IKSNIQAGLNST-----KSGLKNLYLAIPKD--YDPQKGGTLNDFIK 46
                                                                                                                                                                                                                                                                                                                        4 LANISTNLKNSLÓSGLHKTGOSLNQAGOSLKAGAKKLILYIPKDYEYDSGRGNGLODLVK 63
                                                                   The present sequence is protein prod. of the Pasteurella suis leukotoxin gene pslktA, which together with the pslktC, and pslktB prods. comprises a high mol. wt. calcium dependent cytocoxic protein of the repeat of toxin family (RTX), capable of killing both BL-3 cells and pig lymphocytes. The leukotoxin proteins, and the pslktC, A and B genes, or fragments, can be used as immunogens in vaccines for the immunisation of pigs against diarrhoea, or as reagents in diagnostic assays. The leukotoxin genes were isolated by screening a P. suis genomic library, in the phage vector lambda-dash, with a DNA probe derived from pYFC19, a plasmid carrying the IKKCA locus (Chang et al., Infect. Immun., vol. 55, pp2348-2354, 1987).
                                                                                                                                                                                                                                                                                                                                                           SAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYQSTDNLKSVEEVIGSQFND
     for
υσυλυτική genes from Pasteurella suis - also vectors and cells expressing gene prods., for use in vaccines against porcine enteritis
                                                                                                                                                                                                                                                    Query Match

49.4%; Score 2297.5; DB 17; Length 934;
Best Local Similarity 49.7%; Pred. No. 1.1e-134;
Matches 469; Conservative 172; Mismatches 254; Indels 49;
                                                 Claim 34; Columns 59-64; 47pp; English
                                                                                                                                                                                                                                934 AA;
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                                                                                                            GNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRW
VFKGSKFNDI FHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is encoded by the appA gene carried on a 1.8 kb section of clone yfc5 which was isolated by immunological screening. It forms the appCA natigen with the appC arctein encoded on the same section of DNA. The appA antigen is not in itself haemolytic but does elicit an immune response and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
48.1%; Score 2236.5; DB 12; Length 956;
Best Local Similarity 47.7%; Pred. No. 7.4e-131;
Matches 453; Conservative 188; Mismatches 255; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding Actinobacillus pleuropneumoniae haemolysin - used for producing haemolysin antigen for vaccinating pigs against
                                                                                                                                                                                                                                                                                                                                                                      cytotoxin
                                                                                                                                                                                                                                                                                                                                   DENKSQKLSASDIAS-SLNKLVGSMALFGTANSVSSNALQPITQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; porcine pleuroneumonia; haemolysin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinobacillus pleuroneumoniae serotype 5
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pleuropneumoniae infection; swine pleuropneumonia

Actinobacillus pleuropneumoniae

CA2170839-A 02-SEP-1996

therapy; A.

RTX toxins

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Rosendal

Ricciatti P,

MacInnes J, Mallard B, WPI; 1997-245536/23.

N-PSDB; AAT73219

(UYGU-) UNIV GUELPH

95US-0396244.

01-MAR-1996;

Preparations of microorganisms producing cell-associated especially for production of vaccines against swine

pleuro-pneumonia

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    887
         KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK 156
                                                                                                                                                                                | ::| ||::||::| ||::||:|| AGLELTNELVGNIASSVQTVDAFAEQISKLGSHLQNVKGLGGLSNKLQNLPDLGKASLGL
                                                                                                                                                        KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ
                                             ASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL
                                                                                                          EIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST
                                                                                                                                              TGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVG
                                                                                                                                                                                                                      NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD
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                                                                                                                                                                                                                                                                  HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
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                                                                                                                                                                                                                                                                                                                                                                                    ATAETEKGSYSVKRYVGDSKALHETIATHQTNVGNREEKIEYR-REDDRFHTGYTVTDSL
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AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)

toxins. These sequence are encoded by the apxICA, apxIBD, apxIIABC, and

apxIIIABCD genes (see AAT73217-T73220), and can be expressed by

microorganisms used in the preparations of the invention. The

microorganisms used in the preparations of the invention. The

preparations are bacterial preparations comprising one or more RTX

con instance the strains have at least one cell-associated RTX toxin.

The preparations are used for production of vaccines for the prophylaxis

and treatment of infectious diseases caused by microorganisms that

produce RTX toxins, where the strains have been attenuated or

inactivated. The vaccines are preferably against Actinobacillus

pleuropneumoniae infection (swine pleuropneumonia). It has been found

that A. pleuropneumonia produces significant quantities of

cell-associated RTX toxins when cultured under certain conditions, and

that the whole-cell protein profiles obtained from cells recovered at

necropsy from the pleural fluid of infected swine. Vaccination with a

necropsy from the pleural fluid of infected swine. Vaccination with a

certain prepared from heat-inactivated cultures having significant

quantities of cell-associated RTX toxins give significant protection of

swine against challenge with homologous strains.
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48.1%; Score 2236.5; DB 18; Lengt
Best Local Similarity 47.7%; Pred. No. 7.4e-131;
Matches 453; Conservative 188; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Pages 101-104; 151pp; English
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RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production;

(first entry)

16-FEB-1998

AAW22156;

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                                                                                                              331 INQKGEKVRIGNWFLEDDLASTVANYKAT-NDRKIEEIIGKGGERITSEQVDKLI--KEG
TIEASLTTISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVA
                                                                       NRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD
                                                                                                                                                       516 HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
                                                                                                                                                                                                -----ETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVD
                                                                                                                                                                                                            GTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYGTDNL
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passive immunization; clyIIA.
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comparises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYE) broth, which produces one or more RTX toxins, where the strain(s) broth, which produces one or more RTX toxins, where the strain(s) broth, which is call-associated. The products of the invention have immunostimulatory, antimicrobial, antimiflammatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infectious diseases are swine pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in swine; septicemia, nephritis, endocarditis and arthritis in piglets; shipping cerver and abortion in cattle; whooping cough, sleepy foal disease or joint ill (purulent nephritis, arthritis) in foals; septicemia, polyarthritis and abortion in horses; and urinary infections, peritonitis, meningitis, and gastroenteritis. The bacterial preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus pleuropneumoniae clyIIA protein described in the method of the invention.
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                                                                                Bacterial preparation comprising microorganisms which produce a memt of the Repeats in Toxins (RTX) family, useful for treating swine pleuropneumonia, arthritis in swine, shipping fever and abortion in cattle, and sleepy foal disease.
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                                                                                                                                                                                                     invention describes a novel bacterial preparation (I)
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48.1%; Score 2236.5; DB 21; Lengt
Best Local Similarity 47.7%; Pred. No. 7.4e-131;
Matches 453; Conservative 188; Mismatches 255; Indels
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                                                                                                                                                                                                                                                                                                                                                   RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
                 HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
                                          -----ETEGTDEIGLIVNAKAGNDDIFVGQKKNNIDGGDGHDRVFYSKDGGFGNITVD
                                                   DDAGNIIESKDTK---IIANLGAGNDNVFVGSSTTVIDGGDGHDRVHYSR-GEYGALVID
                                                                            GTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYBLRKVGYGYQSTDNL
                                                                                       KSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLL
                                                                                                                        DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVK
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                                                                                                                                                                                                                               producing cell-associated vaccines against swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosendal
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N-PSDB; AAT73220.
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toxins, where the strains have at least one cell-associated RTX toxin.

The preparations are used for production of vaccines for the prophylaxis
and treatment of infectious diseases caused by microorganisms that
produce RTX toxins, where the strains have been attenuated or
inactivated. The vaccines are preferably against Actinobacillus
pleuropneumonia e infection (swine pleuropneumonia). It has been found
that A. pleuropneumonia produces significant quantities of
cell-associated RTX toxins when cultured under certain conditions, and
that the whole-cell protein composition of the cultures corresponds to
the whole-cell protein profiles obtained from cells recovered at
necropsy from the pleural fluid of infected swine. Vaccination with a
bacterin prepared from heat-inactivated cultures having significant
quantities of cell-associated RTX toxins give significant protection of
swine against challenge with homologous strains.
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Best Local Similarity 43.0%; Pred. No. 2.5e-111;
Matches 428; Conservative 152; Mismatches 296;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel bacterial preparation (I) which comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antimicrobial, antimiclammatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which produce one or more RTX toxins. The infectious diseases are swine pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in piglets; shipping fever and abortion in cartle; whooping cough, sleepy foal disease or joint ill (purulent nephritis, arthritis) in foals; septicemia, polyarthritis and abortion in horses; and urinary infections,
                                                                  LEGGDGSDFYVYRSTSGNHTIYDQGKASDSDKLYLSDLSFDNILVKRVNDNLEFRSNNNS 910
                                                                                                                                                                                                                                                                                                                                                        RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial; antiinflammatory; antiarthritic; antiabortive; treatment; pneumonia; pleuropneumonia; septicemia; nephritis; arthritis; endocarditis; shipping fever; abortion; whooping cough; sleepy foal disease; joint ill; urinary infection; peritonitis; meningitis; gastroenteritis;
                          EGDDKLLGGNGNNYLSGGDGNDELQVLGNGFNVLRGGKGDDKLYGSSGSDLLDGGEGNDY 850
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                                                    LNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVK--RND
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of the Repeats in Toxins (RTX) family, useful for treating swine
pleuropneumonia, arthritis in swine, shipping fever and abortion in
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                                                                                                                                                                                                                                                                                                                                   pleuropneumoniae apxIIIA protein.
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passive immunization; apxIIIA.
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peritonitis, meningitis, and gastroenteritis. The bacterial preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus pleuropneumoniae apxIIIA protein described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDG--EASSKLDFSKVIQR-----
                                                                                                                                                        Length 1049;
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                                                                                                                                                    Query Match 41.4%; Score 1924; DB 21; Best Local Similarity 43.0%; Pred. No. 2.5e-111; Matches 428; Conservative 152; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGD-----
                                                                                                                1049 AA;
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429 282 489 342 549 402 609 462 899 518 785

630 844 688 904 739

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964 EGDDKLIGGNGNNYLSGGDGNDELQVLGNGFNVLRGGKGDDKLYGSSGSDLLDGGEGNDY 1023
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             GITKLGERIKSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFT
                                                                                                                                                                                                                                                                                                                                                                                          754 INGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVK--RND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  809 HSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQ
GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                              IGNISOSTOTIEAFSSQLAKLGSTISOAKGFSNIGNKLQNLN---FSKTNLGLEIITGLL
                                                                                                                                         ITSSIMLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLT
                                                                                                                                                                                       343 TISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
                                                                                                                                                                                                  403 LEWEKONGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEVIGSOFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGD-----
                                                                                           SGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAAL
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             959
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(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding Actinobacillus pleuropneumoniae leukotoxin - used prepare prods. for use in vaccines for porcine pleuropneumonia
                                                                                                                                                                                                                           Leukotoxin; AppIIIA; pleuropneumonia; vaccine; diagnostic.
                                                  960 LLKNVTQEQNESNLSS--LKTELGKIITNAGNFGVA 993
                                   ELKKLADENKSQKLSASDIASSLNKLVGSMALFGTA 904
                                                                                                                                                                                                                                                                                                       488..503
/label= transmembrane domain
570..587
/label= transmembrane domain
                                                                                                                                                                                                                                                                                                transmembrane
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                                                                                                                    AAR54781 standard; Protein; 1244
                                                                                                                                                                                                                                                 Actinobacillus pleuropneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-US10500
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93US-0072285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and as diagnostic reagents
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(first entry)
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N-PSDB; AAQ64827.
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15-OCT-1994
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us-10-069-799-5.rag

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791 781 851

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antiinflammatory; antiarthritic; antiabortive; treatment; pneumonia; pleuropneumonia; septicemia; nephritis; arthritis; endocarditis; shipping fever; abortion; whooping cough; sleepy foal disease; joint ill; urinary infection; peritonitis; meningitis; gastroenteritis;
                                                                                                                                                                                                                                                                                        EKNDRIYLSSGSSIVYAGNGHDVAYYDKTDTGY--LTFDGQSAQKAGEYIVTKELKADVK 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;
                                                                                                                                             SFLNVADKFERAKQLEQYSERFKKFGYEGDSLLASFYRETGAIEAALTTINSVLSAASAG
                                                                        RLTNGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNAKAG
                                                                                                                                                                                                                                                                                                                                         --NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-ARGD
                                                                                                                                                                                                                                                                                                                                                                                                                646 IYHEVVKRQETKVGKRTETIQYRDYELR - - KVGYGYQSTDNLKSVEEVIGSQFNDVFKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                  VSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNY
                                                                                                                          FDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSG
                                                                                                                                                                                             KAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             toxins. These sequence are encoded by the apxICA, apxIBD, apxIIABCC genes (see AAT71217-T71220), and can be expressed by microorganisms used in the preparations of the invention. The preparations of the invention. The preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus that A. pleuropneumoniae infection (swine pleuropneumoniae). It has been found that A. pleuropneumonia produces significant quantities of cell-associated RTX toxins when cultured under certain conditions, and the whole-cell protein profiles obtained from cells recovered at necropsy from the pleural fluid of infected swine. Vaccination with a chartities of cell-associated RTX toxins give significant protection of quantities of cell-associated RTX toxins give significant protection of swine against challenge with homologous strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLOKHSTNKLAKGL-DSVENIDRKLGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ASNVLSTLSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQT 175
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                                                                                                                                                                                                                                                                                                                                              toxing
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   A. pleuropneumoniae infection; swine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                             RIX
                                                                                                                                                                                                                                                                                                                                           producing cell-associated vaccines against swine
                                                                                                                                                                                                                                                     Rosendal S;
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Pages 88-91; 151pp; English.
                                                                                                                                                                                                                                                     Ricciatti P,
                                     Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                                                                                                                                                           Preparations of microorganisms - especially for production of
                                                                                                                                               96CA-2170839
                                                                                                                                                                                95US-0396244
                                                                                                                                                                                                                                                     Mallard
                                                                                                                                                                                                                                                                                     WPI; 1997-245536/23.
N-PSDB; AAT73217.
                                                                                                                                                                                                                    GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1022 AA;
                                                                                                                                                                                                                                                                                                                                                                                pleuro-pneumonia
                                                                                                                                                                                                                  (DYGU-) UNIV
                                                                                                                                               01-MAR-1996;
                                                                                                                                                                                01-MAR-1995;
                                                                                                                                                                                                                                                     MacInnes J,
                                                                                                           02-SEP-1996
                                                                          CA2170839-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Matches 40
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WYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADEN 877
                                                                                                         --NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-ARGD
                                                                                                                                                                             NGGDGDDELQVFEGQYNVLLGGAGNDILYGSDGTNLFDGGVGNDKIYGGLGKDIYRYSKE
             KAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRE
                                     RLTNGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNAKAG
                                                                                                                                                                                                                                                    ----KLAFADANI----SDIMIERTKEGIIVKRNDHSG-SINIPR
                                                                                                                                                                                                                            646 IYHEVVKRQETKVGKRTETIQYRDYELR - - KVGYGYQSTDNLKSVEEVIGSQFNDVFKGS
                                                                                                                                                                                                                                                                                                                                                                           DGGSGDD------VLNGGAGNDVY-----IFRKGDGNDTLYDGTGND-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A vaccine contg. a product of the LhaA gene as the active ingredient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat; vaccine; antigenic; immunisation; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSQKLSASDIASSLNKLVGSMALF-GTANSVSSNALQPI 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to ATT codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note = "corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LhaA (low homology to appA) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR76991 standard; Protein; 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                       KFNDI FHSGEGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-228639/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease
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                                                                                                                                                                                                                                                                             This invention describes a novel bacterial preparation (1) which comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TTE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antiarthritic and antiabortive activity.

CT he bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infectious diseases are swine pleurophneumonia, pneumonia, septicimia, nephritis and arthritis in swine; septicemia, nephritis, endocarditis and arthritis in swine; septicemia, nephritis, and astruction in cattle; whooping cough, aleepy foal disease or joint ill (purulent nephritis, arthritis) in foals; septicemia, perparations cough, also preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 SFLNVADKFERAKQLEQYSERFKKFGYEGDSLLASFYRETGAIEAALTTINSVLSAASAG 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 IEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGAAATGSLVGAPVAALVSAITGIISGILDASKQAIFERVATKLANKIDEWEKKH-GKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 FÜKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSG
                                                                                                                                                          tterial preparation comprising microorganisms which produce a memt
the Repeats in Toxins (RTX) family, useful for treating swine
suropneumonia, arthritis in swine, shipping fever and abortion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 1022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
37.9%; Score 1763.5; DB 21; Length 1022
Best Local Similarity 40.0%; Pred. No. 2.4e-101;
Matches 400; Conservative 181; Mismatches 309; Indels 109;
                                                                     Ricciatti
                                                                                                                                                                                                                                                      Disclosure; Column 47-52; 96pp; English
                                                                     MacInnes J,
                                                                                                                                                                                               pleuropneumonia, arthritis in sw
cattle, and sleepy foal disease
 95US-0396244
                                                                     Rosendal
                                                                                                         WPI; 2000-146864/13
                                 (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1022 AA;
                                                                                                                          N-PSDB; AAZ88584
01-MAR-1995;
                                                                     Mallard B,
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--KLAFADANI----SDIMIERTKEGIIVKRNDHSG-SI
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                                                                                                                                                                                                                                                                                                                                                                     Lee RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.5%; 8
                                                                                                                                                                                                                animal feed; mutant; mutein.
                                                                                                                                                                                                                                                                                                           15-DEC-2000; 2000WO-CA01498.
                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                  (UYGU-) UNIV GUELPH OFFICE.
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                    Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-408470/43
                                                                                                                                                                                                                                                                                                                                                                      Shewen PE,
                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608 AA;
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                                                                                                                                                                                                                                                                  WO200144289-A2
                                                                                                                                                                                                                                                                                                                              17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 290;
                                                                                                                                                    10-SEP-2001
                                                                                                                                                                                                                                                                                      21-JUN-2001
                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                 AAE04636;
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782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 KAG--NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-A 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFGSRFTDIFHGAKGDDEIYGNDGHDILYGDDGNDVIHGGDGNDHLVGGNGNDRLIGGKG 788
                                                                                                                                                                                                                                                                                                IEAFSSQLAKLGS---TISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFAL 231
                                                                                                                                                                                                                                                                                                                                                                                 SPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERI 471
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                                                                                                                                                                                     PKGSKFNDIFHSGEGD--------DLLDGGAGDDRLFGGKGNDRLSGDEG
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                                                                                                                                                                        ----KNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
                                                                                                                                                                                                                                                                                                                                        ADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAI
                                                                                                                                                     Gaps
                                              AAR76991 represents the lhaA (low homology to appA) gene product. The lhaA protein (which is a toxin component and contains a repeat region) and fragments of this protein are useful as the active ingredient in vaccines for the prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae infectious (Apl) diseases.
prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae
                                                                                                                                                    112;
                                                                                                                                Length 1023;
                                                                                                                                                    Indels
                                                                                                                                 DB 16;
                                                                                                                                7.2%; Score 1727; DB 16; Local Similarity 41.4%; Pred. No. 4.6e-99; Nes 390; Conservative 169; Mismatches 271;
                            Claim 3; Page 8-11; 15pp; Japanese
                                                                                                                                                                        KSNIQAGLNSTKSGL-
          diseases
                                                                                                            1023 AA;
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849 YSKEYGRHIIIEKGGDDDTLLLSDLSFKDVGFIRIGDDLLVNKRIGGTLYYHEDYNGNAL 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunostimulant; antibacterial; vaccine; transgenic plant;
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Pred. No. 5.3e-83;
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Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic
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                                         GIELDNAGNVTKTKETKIIAKLGEGDDNVFVGSGTTEIDGGEGYDRVHYSR-GNYGALTI
                                                                                                             DATKETEQGSYTVNRFVETGKALHEVTSTHTALVGNREEKIEYR-HSNNQHHAGYYTKDT
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 QRWDNN1GELAGITKLGER1KSGKAYADAFEDGKKVEAGSNITLDAKTGI1D1SNSNGKK
        TOALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRV
                                                                  -----ABTEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITV
                                                                                                   DGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDN
                                                                                                                                    LKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDL
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N-PSDB; AAT08098.
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colitis, haemolytic uremic syndrome and mesenteric adenitis have been found to carry a hlyk gene and a hyla gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so sprovide a useful target for detecting EHEC pathogens, esp. 0157:H7 serotype E.coli. The present sequence is that of the protein encoded by the EHEC hlyA gene.
                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                            Query Match 29.6%; Score 1376.5; DB 17; Lengt Best Local Similarity 40.5%; Pred. No. 2.2e-77; Matches 304; Conservative 129; Mismatches 225; Indels
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Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
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                                                            Pasteurella haemolytica modified leukotoxin 50 (1kt50) protein.
                                                                                           Leukotoxin 50; lkt50; respiratory disease; infection; therapy; immunostimulant; antibacterial; vaccine; transgenic plant; animal feed; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                          Strommer JN;
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                                                                                                                                                           Pasteurella haemolytica
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N-PSDB; AAD08976.
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AAE04637;
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                                                                                    Novel Moraxella bovis antigen useful in compositions for raising immune response in an animal, has protease, lipase or hemolysin activity
                                                                                                                                                                          The invention relates to new Moraxella bovis antigens and nucleic acid sequences encoding these antigenic polypeptides. The antigenic polypeptides and polymucleotides are useful for raising an immune response in an animal directed against Moraxella, preferably against M. bovis or M. catarrhalis, and for treating Moraxella infections. The present sequence represents the amino acid sequence of the A subunit of the RTX toxin from M. bovis Dalton 2d.
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Human ORFX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial; A subunit
 Moraxella bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200116172-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1999;
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360

RESULT 1

AAB621.

480

480 540 540 600 600 99 099 720 720

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Gaps

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RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                  Preparations of microorganisms producing cell-associated RTX toxins - especially for production of vaccines against swine pleuro-pneumonia
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 107-110; 151pp; English.
                     AAW22159 standard; Protein; 1049 AA.
                                                                                                                                                   Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                    96CA-2170839
                                                                                                                                                                                                                                          95US-0396244
                                                              (first entry)
                                                                                                                                                                                                                                                                                      Mallard B,
                                                                                                                                                                                                                                                                                                         WPI; 1997-245536/23.
N-PSDB; AAT73220.
                                                                                                                                                                                                                                                                (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 AA;
                                                                                     ApxIIIB protein.
                                                                                                                                                                                                                     01-MAR-1996;
                                                                                                                                                                                                                                          01-MAR-1995;
                                                                                                                                                                                                                                                                                      MacInnes J,
                                                               16-FEB-1998
                                                                                                                                                                           CA2170839-A.
                                                                                                                                                                                               02-SEP-1996
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                                           AAW22159;
           AAW22159
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840
                                                     840
                                                                                     Enterohaemorrhagic Escherichia coli; virulent; EHEC; 0157:H7 serotype; detection; probe; primer; hlyA gene; enterohaemorrhagic colitis; haemolytic uremic syndrome; mesenteric adenitis.
                                             DKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLI
                                                                           GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMAL
                                 DKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterohaemorrhagic E.coli (EHEC) associated with enterohaemorrhagic colitis, haemolytic uremic syndrome and mesenteric adentitis have been found to carry a hlyA gene and a hylB gene, separated by an intergenic region. The hly genes and the intergenic region are absent from bacteria not associated with these diseases and so provide a useful target for detecting EHEC pathogens, esp. 0157:H7 encoded by the EHEC hlyA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Entero:haemorrhagic E. coli (EHEC) nucleic acid sequences - useful for probe and primer design for sensitive and specific detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 758;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.5%; Score 14; DB 17; I 100.0%; Pred. No. 0.00048; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                Enterohaemorrhagic E.coli hlyA gene product.
                                                                                                                     FGTANSVSSNALQPITQPTQGILAPSV 927
                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Columns 37-42; 32pp; English
                                                                                                                                                                                                                                                                                                                                 Escherichia coli (enterohaemorrhagic)
                                                                                                                                                                                                 AAR86998 standard; Protein; 758 AA
                                                                                                                                                                                                                                                                                                                                                                                                94US-0258188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
Best Local 14/ Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 ISGILEASKQAMFE 392
                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0258188
                                                                                                                                                                                                                                          (first entry)
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N-PSDB; AAT08098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hall RH, Xu JG;
                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUN-1994;
                                                                                                                                                                                                                                            04-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1995.
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            721
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Rosendal S;

Ricciatti P,

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contains. These sequence are encoded by the apxICA, apxIBA, apxIBA, apxIIABCC and apxIIABCD genes (see AAT73217-T73220), and can be expressed by microorganisms used in the preparations of the invention. The microorganisms used in the preparations of the invention. The preparations are bacterial preparations of the invention. The cand purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus pleuropneumoniae infection (swine pleuropneumonia). It has been found that A. pleuropneumonia produces significant quantities of that A. pleuropneumoniae infection (swine pleuropneumonia). It has been found that the whole-cell protein composition of the cultures corresponds to the whole-cell protein composition of the cultures corresponds to the whole-cell protein composition of the cultures corresponds to the whole-cell protein fluid of infected swine. Vaccination with a necropsy from the pleural fluid of infected swine. Vaccination with a guantities of cell-associated RTX toxins give significant protection of swine against challenge with homologous strains.
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AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY51412 standard; protein; 1049 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%; Scc...
100.0%; Pre
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Best Local Similarity 100.
Matches 14; Conservative
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ID AAYS
XX
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152 İSGİLEASKQAMFE 165

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The AppIIIA gene having the sequence given in AAQ64827 was isolated from phage lambda clones yfc 26-28 and yfc 31-32 of a genomic library of A. pleuropneumoniae ser. 2. The gene encodes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding Actinobacillus pleuropneumoniae leukotoxin - used prepare prods. for use in vaccines for porcine pleuropneumonia and as diagnostic reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 14; DB 15; Length 1244; 00.0%; Pred. No. 0.00075; ve 0; Mismatches 0; Indels 0
                                                                                                                                          Leukotoxin; AppIIIA; pleuropneumonia; vaccine; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccine; porcine pleuroneumonia; haemolysin; cytotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leukotoxin (sequence AAR54781).
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                  /label= transmembrane domain 570..587
                                                                                                                                                                                                                                                                                                                                               /label= transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPA haemolysin antigen encoded by appA.
                                                                                                                                                                                                                                             327..345
/label= transmembrane
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR12561 standard; Protein; 956 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 3; 65pp; English.
                                                                                                                                                                                 Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93WO-US10500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0972229.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 KVAAGFELSNQVIG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVAAGFELSNOVIG 461
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (updated)
(first entry)
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                   488..503
                                        (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-167130/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1244 AA;
                                                                                                  Leukotoxin AppIIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ64827
                                                                                                                                                                                                                                                                                                                                                                                       WO9409821-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1992;
03-JUN-1993;
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26-JUL-1991
                                    25-MAR-2003
15-OCT-1994
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AAR54781;
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                                                                                                                                                                                                                         Key
Domain
                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises one or more isolated and purified strain(s) of a microorganism, comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antimurcobial, antihilammatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophlaxis and transment of infectious diseases caused by strains of microorganisms transment of infectious diseases caused by strains of microorganisms of the prophlaxis and archritis and archritis in swine pleuropneumonia, pneumonia, septicemia, nephritis, endocarditis and arthritis in piglets; shipping septicemia, nephritis, endocarditis and arthritis in piglets; shipping fever and abortion in cattle; whooping cough, sleepy foal disease or joint ill (purulent nephritis, arthritis) in foals; septicemia, polyarthritis and abortion in horses; and urinary infections.

Compassive immunization. This sequence represents the Actinobacialus may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacialus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                        antiinflammatory; antiarthritic; antiabortive; treatment; pneumonia; pleuropneumonia; septicemia; nephritis; arthritis; endocarditis; shipping fever; abortion; whooping cough; sleepy foal disease; joint ill; urinary infection; peritonitis; meningitis; gastroenteritis;
                                                                                                                         RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   пешрег
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacterial preparation comprising microorganisms which produce a memb
of the Repeats in Toxins (RTX) family, useful for treating swine
pleuropneumonia, arthritis in swine, shipping fever and abortion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes a novel bacterial preparation (I) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  passive immunization. This sequence represents the Actinobacill pleuropneumoniae apxIIIA protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MacInnes J, Ricciatti P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 21; I
Pred. No. 0.00064;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 77-84; 96pp; English.
                                                                                 A. pleuropneumoniae apxIIIA protein.
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cattle, and sleepy foal disease -
                                                                                                                                                                                                                                                                  Actinobacillus pleuropneumoniae.
                                                                                                                                                                                                      urinary infection; peritonitis
passive immunization; apxIIIA.
                                                                                                                                                                                                                                                                                                                                                                                          96US-0772270
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                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mallard B, Rosendal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-146864/13.
N-PSDB; AAZ88587.
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es 14; Conserv
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                                        05-MAY-2000
                                                                                                                                                                                                                                                                                                           US6019984-A.
                                                                                                                                                                                                                                                                                                                                                 01-FEB-2000
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    AAY51412;
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Gaps

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Actinobacillus pleuroneumoniae serotype 5.

AAR54781 standard; Protein; 1244 AA.

RESULT 5 AARS4781 ID AAR

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Matches

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RIX toxin, vaccine, Repeats in Toxins, immunostimulatory, antimicrobial, antiinflammatory; antiarthritic, antiabortive, treatment; pneumonia; pleuropneumonia; septicemia; nephritis; arthritis; endocarditis; shipping fever; abortion; whooping cough; sleepy foal disease; joint ill; urinary infection; peritonitis; meningitis; gastroenteritis;
                                                                                                 AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins) toxins. These sequence are encoded by the apxICA, apxIBD, apxIIAB'C, and apxIIABD genes (see AAT72217-T73220), and can be expressed by microorganisms used in the preparations of the invention. The preparations are bacterial preparations comprising one or more isolated and purified strains of a microorganism that produces one or more RTX toxins, where the strains have at least one cell-associated RTX toxin. The preparations are used for production of vaccines for the prophylaxis and treatment of infectious diseases caused by microorganisms that
                                                                                                                                                                                                                                                                                      produce RTX toxins, where the strains have been attenuated or inactivated. The vaccines are preferably against Actinobacillus pleuropneumoniae infection (swine pleuropneumonia). It has been found that A. pleuropneumonia produces significant quantities of cell-associated RTX toxins when cultured under certain conditions, and that the whole-cell protein composition of the cultures corresponds to necropsy from the pleural fluid of infected swine. Vaccination with a bacterin propared from heat-inactivated cultures having significant quantities of cell-associated RTX toxins give significant protein profession with a partities of cell-associated RTX toxins give significant protection of swine against challenge with homologous strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial preparation comprising microorganisms which produce a member of the Repeats in Toxins (RTX) family, useful for treating swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 11; DB 18; Length 956;
Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
  especially for production of vaccines against swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricciatti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%; Scc.
100.0%; Pred. No. v..
                                                             Disclosure; Pages 101-104; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MacInnes J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A. pleuropneumoniae clyIIA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY51410 standard; protein; 956 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinobacillus pleuropneumoniae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           urinary infection; peritoniti
passive immunization; clyIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0396244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 ALLVAGVTGLI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 ALLVAGVIGLI 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-146864/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      956 AA;
                   pleuro-pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ88586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6019984-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is encoded by the appA gene carried on a 3.8 kb section of clone yfc5 which was isolated by immunological screening. It forms the appCA antigen with the appC protein encoded on the same section of DNA. The appA antigen is not in itself haemolytic but does elicit an immune response and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                DNA encoding Actinobacillus pleuropneumoniae haemolysin - used for producing haemolysin antigen for vaccinating pigs against porcine pleuro-pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 11; DB 12; Length 956;
100.0%; Pred. No. 0.43;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricciatti P, Rosendal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW22156 standard; Protein; 956 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacillus pleuropneumoniae.
                                                                                                                                                                 (TEXA ) UNIV TEXAS A & M SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Fig 1; 28pp; English.
                                                                                                                         89US-0429273.
                                                                                   90WO-US06350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ALLVAGVTGLI 379
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                                                                                                                                                                                                         Struck DK, Young RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MacInnes J, Mallard
                                                                                                                                                                                                                                                   WPI; 1991-164202/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-245536/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        956 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR12127
                                                                                                                                                                                                                                                                           N-PSDB; AA011873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ApxIIC protein.
                                                                                                                         31-OCT-1989;
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WO9106653-A
                                       16-MAY-1991
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccines
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Gaps

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RTX toxin; vaccine; Repeats in Toxins; immunostimulatory; antimicrobial; antiniflammatory; antiarthritic; antiabortive; treatment; pneumonia; pleuropneumonia; septicemia; nephritis; arthritis; endocarditis; shipping fever; abortion; whooping cough; sleepy foal disease; joint ill; urinary infection; peritonitis; meningitis; gastroenteritis; passive immunization; apxIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial preparation comprising microorganisms which produce a memb
of the Repeats in Toxins (RTX) family, useful for treating swine
pleuropneumonia, arthritis in swine, shipping fever and abortion in
AAW22151-W22161 represent A. pleuropneumoniae RTX (repeat in toxins)
                                                                                                                                                                                                                                                                                                                1.2%; Score 11; DB 18; Length 1022;
100.0%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MacInnes J, Ricciatti P;
                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. pleuropneumoniae apxIA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cattle, and sleepy foal disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus pleuropneumoniae.
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                                                                                                                                                                                                                                                                                                                    Query Match 1.2
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                       266 AQRVAAGLSTT 276
                                                                                                                                                                                                                                                                                                                                                                                       Rosendal S,
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                                                                                                                                                                                                                                                                                        1022 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY51406;
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51406
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                                                                  This invention describes a novel bacterial preparation (1) which comprises one or more isolated and purified strain(s) of a microorganism, contribed in tryptone yeast extract (TTE) broth, which produces one or cultured in tryptone yeast extract (TTE) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is coll-associated. The products of the invention have immunostimulatory, antiarthritic and antiabortive activity. The bacterial preparation may be used as vaccines for the prophylaxis and treatment of infectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infectious diseases are swine pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in swine; septicemia, nephritis, endocarditis and arthritis in piglets; shipping tever and abortion in cattle; whooping cough, alsepy foal disease or joint ill (purulent nephritis, and gastroenterius, fibe bacterial, preparations may also be used to prepare antibodies which may be used as a means of may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacillus preparation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTX toxin; apxICA gene; apxIBD gene; apxIIAB'C gene; apxIIIABCD gene; repeat in toxins toxin; cell-associated RTX toxin; vaccine production; therapy; A. pleuropneumoniae infection; swine pleuropneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparations of microorganisms producing cell-associated RTX toxins - especially for production of vaccines against swine pleuro-pneumonia
     pleuropneumonia, arthritis in swine, shipping fever and abortion in cattle, and sleepy foal disease
                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                           1.2%; Score 11; DB 21; Length 956;
100.0%; Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricciatti P, Rosendal
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                               Disclosure; Column 67-72; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW22152 standard; Protein; 1022 AA.
                                                                                                                                                                                                                                                                                                                                                                             1.22,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  369 ALLVAGVTGLI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ALLVAGVTGLI 402
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nes 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-245536/23.
N-PSDB; AAT73217.
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                                                                                                                                                                                                                                                                                                                                                     956 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ApxIA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                      Sequence
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Matches
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This invention describes a novel bacterial preparation (1) which comprises one or more isolated and purified strain(s) of a microorganism, cultured in tryptone yeast extract (TYP) broth, which produces one or more RTX toxins (belonging to the family of toxins referred to as Repeats in Toxins), where the strain(s) have at least one RTX toxin which is cell-associated. The products of the invention have immunostimulatory, antimurication land antiabortive activity, antimicrobial, antiinflammatory, antiarthritic and antiabortive activity.

The bacterial preparation may be used as vaccines for the prophylaxis and control in frectious diseases caused by strains of microorganisms which produce one or more RTX toxins. The infections diseases are swine pleuropneumonia, pneumonia, septicemia, nephritis and arthritis in piglets; shipping fever and abortion in cattle; whooping cough, sleepy foal disease or joint ill (purulent nephritis, arthritis) in foals; septicemia, pepticinis, and gastroomteritis. The bacterial preparations may also be used to prepare antibodies which may be used as a means of passive immunization. This sequence represents the Actinobacique.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pleuropneumoniae apxIA protein described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2%; Score 11; DB 21; Length 1022; 0.0%; Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTX; repeat; vaccine; antigenic; immunisation; pneumonia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note = "corresponds to ATT codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LhaA (low homology to appA) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinobacillus pleuropneumoniae.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            289 AQRVAAGLSTT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 AQRVAAGLSTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-228639/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP07138185-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ар1 dівеаве.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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AAR76991 represents the lhaA (low homology to appA) gene product. The lhaA protein (which is a toxin component and contains a repeat

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-50 (lkt50) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a ruminant, to prevent or treat respiratory diseases.
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                Pasteurella haemolytica modified leukotoxin 50 (1kt50) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                            Leukotoxin 50; lkt50; respiratory disease; infection; therapy; immunostimulant; antibacterial; vaccine; transgenic plant; animal feed; mutant; mutein.
region) and fragments of this protein are useful as the activingredient in vaccines for the prophylaxis of Actinobacillus (Haemophilus) pleuropneumoniae infectious (Ap1) diseases.
                                                                                                   Length 1023,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.1%; Score 10; DB 22; Length 450; Best Local Similarity 100.0%; Pred. No. 1.9; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strommer JN;
                                                                                                 DB 16;
0.46;
                                                                                               1.2%; Score 11; DB 3
100.0%; Pred. No. 0.44
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodgins D,
                                                                                                                                                                                                                                                                                   AAE04637 standard; Protein; 450 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 12; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-2000; 2000WO-CA01498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0172148.
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                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                               Query Match
Best Local Similarity 100.0
Matches 11; Conservative
                                                                                                                                                                                     289 AQRVAAGLSTT 299
                                                                                                                                                                  266 AORVAAGLSTT 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-408470/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lo RYC, Shewen PE,
                                                                  1023 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB, AAD08976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200144289-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                   10-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                   AAE04637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease
                                                                                                                                                                                                                                                  RESULT 12
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RESULT 13

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AAY33929

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Chimera; pCB111; LKT 111; GnRH; Gonadotropin releasing hormone; multimer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A chimeric protein (AAM03943) is composed of a fusion between a truncated leukotoxin (LKT-111) from Pasteurella haemolytica and a 4-copy gonadoliberin-releasing hormone (GnRH) repeat sequence (see also AAM03944). It is the product of a chimeric gene (AAT37177) produced by deleting an approx. 1300 bp sequence from pCB113 (see also AAT37176) coding for amino acids 352-784 of LKT-352. Recombinant plasmid pCB111 (LKT 111:4 copy GnRH, ATC 6948) was obtd. Escherichia coli transformants produced the chimeric protein, which is useful as a vaccine for fertility control, esp. immunological sterilisation of domestic or farm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gonadotropin-releasing hormone multimer fusion proteins - with leukotoxin polypeptide for increased immunogenicity, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 10; DB 17; Length 544; 100.0%; Pred. No. 2.3; ative 0; Mismatches 0; Indels
                                                                                                     Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH; fusion protein; immunogen; vaccine; fertility control;
                                                                                                                                                                                        Chimeric Pasteurella haemolytica Al strain B122;
                                                                                                                                                                                                                                                                                                                   494..544
/label= GnRH repeat domain
                                                             LKT-GnRH protein fusion from pCB111.
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW79570 standard; Protein; 544 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 7A-7E; 87pp; English
                                                                                                                                                   contraceptive; sterilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-CA00049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0387156.
                                                                                                                                                                                                                                                                          1..493
/label= LKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                   20-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKT-GnRH chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 LAQRVAAGLS 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Manns JG, Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-384447/38.
N-PSDB; AAT37177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                              Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW79570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animals
                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                   Domain
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides myostatin peptides consisting of 3-100 amino acids, derived from a region of mouse, rabbit, human, baboon, bovine, cacids, christ, turkey or zebrafish myostatin (see sequences AAY33930-939). The myostatin peptides are derived preferably from a region of amino acid residues 1-275, 25-300, 50-325 or 75-350 of the above sequences. The peptides and the nucleic acids encoding the peptides are useful as vaccines for eliciting an immune response in a vertebrate against a myostatin immunogen. They result in increasing body weight.

Wuscle mass, number and size of muscle cells, muscle strength, mammary gland tissue, lactation, appetite or feed uptake, life span of the vertebrate, and cause a reduction in body fat content, useful for muscle wasting conditions. The vaccines are also useful for treating a disorder which comprises degeneration or wasting of muscle in a vertebrate, and cuseful for modulating GDF11 activity. The present sequence represents a leukotoxin carrier protein (LKT 14) which is used as an immunological carrier protein to form a myostatin immunoconjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                       Myostatin; mouse; rabbit; human; baboon; bovine; porcine; ovine; chick; turkey; zebrafish; immune response; vaccine; body weight; muscle mass; mammary gland tissue; lactation; feed uptake; muscle degeneration; GDFII activity; LKT 114; leukotoxin carrier protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New myostatin peptide, multimers and immunoconjugates for eliciting
an immune response in a vertebrate against a myostatin immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                  Leukotoxin carrier protein (LKT 114).
                                                                                                       AAY33929 standard; Protein; 490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW03943 standard; Protein; 544 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-CA00128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0075213
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 LAQRVAAGLS 274
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11 AERVIAITOO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barker CA, Morsey M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-527471/44.
N-PSDB; AAX99361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOS-) BIOSTAR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         WO9942573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-FEB-1998;
                                                                                                                                                                                        09-NOV-1999
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                                                                                                                                                 AAY33929;
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Gaps

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RESULT 14 AAW03943 Strommer JN,

Hodgins D,

Lee RWH,

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(UYGU-) UNIV GUELPH OFFICE
                   Lo RYC, Shewen PE,
                                     WPI; 2001-408470/43.
N-PSDB; AAD08975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9806848-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manns JG,
                                                                                               disease -
                                                                                                                                                                                                                                                                                                                                                                                                AAW79573;
                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                          RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                       The present sequence represents the LKT-GnRH chimeric protein from pCB111. This plasmid contains the LKT 111 polypeptide fused to four copies of the GnRH peptide. This chimera lacks cytotoxic activity which enables there to be an increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated LKT to be expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukotoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammanry tumours in a mammalian individual.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                             Chimeric protein of leukotoxin and gonadotropin releasing hormone useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals
 cytotoxic activity; antigen presentation; immune response; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasteurella haemolytica modified leukotoxin 66 (lkt66) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukotoxin 66; lkt66; respiratory disease; infection; therapy; immunostimulant; antibacterial; vaccine; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 10; DB 19; Length 544;
100.0%; Pred. No. 2.3;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Disclosure; Figure 7.1-5; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE04636 standard; Protein; 608 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal feed; mutant; mutein.
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                                                                                      97WO-CA00559.
                                                                                                          96US-0694865
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                                                                                                                            (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              265 LAGRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella haemolytica
                                                                                                                                                Potter AA;
                                                                                                                                                                    WPI; 1998-159540/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 LAQRVAAGLS
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                      544 AA;
                                                                                                                                                                             N-PSDB; AAV61532
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                                                 WO9806848-A1
                                                                                      08-AUG-1997;
                                                                                                          09-AUG-1996;
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                                                                    19-FEB-1998.
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                                                                                                                                                Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE04636;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
             tumour.
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 16
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Chimera, pCB122; LKT 111; GnRH; Gonadotropin releasing hormone; multimer; cytotoxic activity; antigen presentation; immune response; vaccine;
Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
                                                                                                                                                                                                                                                           The present sequence is Pasteurella (Mannheimia) haemolytica modified leukotoxin-66 (lkt66) protein. The modification comprises the removal of amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Furthermore, the plant transformed with modified leukotoxin sequences is fed to an animal such as a ruminant, to prevent or treat respiratory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric protein of leukotoxin and gonadotropin releasing hormone useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; Score 10; DB 22; Length 608; 100.0%; Pred. No. 2.5; Live 0; Mismatches . 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Figure 9.1-6; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW79573 standard; Protein; 695 AA.
                                                                                                                                                                                                   Claim 2; Fig 2; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKT-GnRH chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AERVIAITQQ 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             443 AERVIAITQQ 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-159540/14.
N-PSDB; AAV61535.
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releasing hormone (GRRH) immunogens and a Pasteurella
haemolytica leukotoxin (LKT) protein. The fusion protein comprises, in
the N to C-terminal direction, a synthetic peptide sequence (AAY58364),
an eight copy GRRH multimer (composed of two copies of the 4xGRRH
autliner sequence of AAY58363), the LKT protein (Which functions as a
carrier protein), and a second eight copy GRRH multimer. The fusion
protein may be used in a vaccine composition for prepubertal
administration to a vertebrate subject to result in prolonged suppression
of reproductive behaviour and/or fertility. GRRH immunospens, analogues or
antibodies that cross-react with endogenous GRRH of a vertebrate subject
are used to manufacture a composition or vaccine for immunosterilisation
The present sequence represents the LKT-GnRH chimeric protein from pCB122. This plasmid contains the LKT 111 polypeptide fused to sixteen copies of the GnRH peptide, in the pattern of: 8 copies of GnRH-LKT 111-8 copies of GnRH-LKT 111-8 copies of GnRH-LKT 111-8 copies of GnRH-LKT 111-8 immered of GnRH increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated into the expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukokoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukotoxin; gonadotropin-releasing hormone; GnRH; immunosterilisation;
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone immunogens, analogues or antibodies used to manufacture vaccines for suppression of reproductive behavior and fertility in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunocontraception; vaccine; feline; canine; equine; cervine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leukotoxin/gonadotropin-releasing hormone fusion protein.
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                 Score 10; DB 19;
Pred. No. 2.9;
                                                                                                                                                                                                                                                   1.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                          mammary tumours in a mammalian individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Fig 6A-6F; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY58361 standard; Protein; 695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Pasteurella haemolytica.
Chimeric - Mammalia.
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99US-0306689
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Best Local Similarity luv...
Best Local 10; Conservative
                                                                                                                                                                                                                                                                                                                                               265 LAQRVAAGLS 274
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                                                                                                                                                                                                                               695 AA;
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06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY58361;
                                                                                                                                                                                                                                 Sequence
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This sequence represents a chimeric gonadotropin releasing

hormone (GnRH)-leukotoxin (LKT) fusion protein, which may be

used as a vaccine. The LKT portion of the protein acts to enhance

the immunogenicity of the multimeric GnRH portion (AAYSB135). The

invention relates to a method of using two GnRH immunogen vaccines to

produce uncastrated male animals for meat production, one vaccination

prior to or during the fattening period to reduce circulating

testosterone levels, and the second vaccination about 2-8 weeks before

catosterone levels, and the second vaccination about 2-8 weeks before

catosterone levels, and the second vaccination about 2-8 weeks before

catosterone levels and the second vaccination about 2-8 weeks before

catosterone levels and the second vaccination to the non-androgenic

stanght gain and muscle/fat distribution of male animals without the

problems associated with male animals. Such problems include "boar

problems associated with male animals. Such problems include "boar

cating," a winnel-like adour found in cooked meat of uncastrated pigs which

is caused by steroids stored in the tissues, and similar flavour

impairments in the meat of other intact male animals. The invention is
                                                                                                                                                                                                                                                                      ö
               The vaccines are used to suppress reproductive behaviour and/or fertility for at least 10 months. The prepubertal administration results in a prolonged, long-term suppression of testicular development and/or function in males, or a prolonged, long-term suppression of ovarian development and/or function in females. The methods provide a viable and desirable alternative to surgical forms of sterilisation that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gonadotropin releasing hormone; GnRH; leukotoxin; LKT; fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody; immunogenic; chimeric; vaccine; testosterone; androgenic; non-androgenic; steroid; reduction; weight gain; muscle distribution; fat distribution; male pattern; boar taint; flavour; impairment;
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                           1.1%; Score 10; DB 21; Length 695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gonadotropin releasing hormone-leukotoxin fusion protein.
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reliable; immunocastration; meat production.
                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY58133 standard; Protein; 695 AA.
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                                                                                                                                                                                                                                               100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Mammalia
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                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                 are currently used
                                                                                                                                                                                      695 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY58133;
                                                                                                                                                                                        Sequence
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LKT; vaccine; antigen; respiratory disease; shipping fever pneumonia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pasteurella haemolytica proteins and genes - used for producing vaccines to protect animals esp. cattle from respiratory diseases e.g. pneumonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus somnus; immunogenic; haemolysin; LppB; LppC;
thromboembolic meningoencephalitis; septicaemia; arthritis;
pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.1%; Score 10; DB 12; Length 924; 00.0%; Pred. No. 3.7; 0; Indels ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawman MJP;
                                                                                                                                             Leukotoxin 352 encoded by plasmid pAA352
                                                                                                                                                                                                                        Pasteurella haemolytica Al strain B122.
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                                 AAR10889 standard; Protein; 924 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potter AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 5; 87pp; English.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acres SD, Babiuk LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .19/1600001-0001; IBB1-0101.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ10272
                                                                                                                                                                                                                                                                                                                                      06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                           07-APR-1989;
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                                                                                                            11-APR-1991
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                                                                    AAR10889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeuticia and pharmaceutical furge. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
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100.0%; Pred. No. 3.3;
ive 0; Mismatches 0; Indels
                                                                      Score 10; DB 21; Length 695;
Pred. No. 2.9;
                                                                                                            0; Indels
more reliable than prior art immunocastration techniques
                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 30246
                                                                                                            Mismatches
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                                                                    Query Match
1.1%; Sco
Best Local Similarity 100.0%; Pr
Matches 10; Conservative 0;
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 100.
Matches 10; Conservative
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                                     695 AA
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ABB67818

ABB6

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The hmb gene encoding the haemin-binding protein was expressed in B. coll as a fusion to the Pasteurella haemolytica leukotoxin gene lkt coded for by plasmid pA352. The hmb gene fragment was taken from pRAP504 and starts at the codon for the 33 rd amino acid residue of ORFI. The haemin binding protein can be used in vaccines for preventing or treating H. somunus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                                         Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and LppC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus somnus; immunogenic; haemolysin; LppB; LppC; thromboembolic meningoencephalitis; septicaemia; arthritis; pneumonia; lktA gene; haemin-binding protein; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.1%; Score 10; DB 14; Length 924;
100.0%; Pred. No. 3.7;
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92US-0893424.
92US-0893426.
93US-0038287.
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                                                                              (UYSA-) UNIV SASKATCHEWAN
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                                                                                                         Harland RJ, Pierrand, Theisen M;
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                                                                                                                                                                                                          WPI; 1993-351733/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    924 AA;
                                                                                                                                                                                                                                      N-PSDB; AAQ51082
                                                                                                                                                                                                                                                                                                                                            and corresp. DNA
29-MAR-1993;
                        29-MAR-1993;
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29-MAR-1993;
29-MAR-1993;
29-MAR-1993;
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04-JUN-1992;
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19-APR-1994
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Rioux C, Theisen M;
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See also AAR42370-86.
(Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                            92US-0865050.
92US-0893424.
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93US-0038719.
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(first entry)
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Les 10; Conservative
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N-PSDB; AAQ51086.
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04-JUN-1992;
04-JUN-1992;
29-MAR-1993;
                                                                           05-APR-1993;
                                                                                                                                                                                                                                                              29-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9321323-A1
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                     28-OCT-1993
                                                                                                                                                                                  04-JUN-1992
                                                                                                                                                                                                             29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
19-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR42380;
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Best Loc Matches

ઠે ద RESULT 23 AAR42380

HERE REAL ENDINE SERVICE SERVI

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See also AAR14481, 83,84 and 85.
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92US-0960932
                                                                                                                                    Query Match
Beet Local Similarity 100.vv
Beet Local Similarity 100.vv
                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYSA-) UNIV SASKATCHEWAN.
                                                                                           fever pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Potter AA,
                                                                                                                                                                                           265 LAQRVAAGLS 274
                                                                                                                                                                                                               256 LAORVAAGLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-152482/18.
N-PSDB; AAQ41317.
                                                                                                                           926 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9308290-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hughes HPA,
                                                                                                                                                                                                                                                                                                               25-MAR-2003
23-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1993
                                                                                                                                                                                                                                                                                           AAR34545;
                                                                                            shipping
                                                                                                                            Seguence
                                                                                                                                                                                                                                                RESULT 26
                                                                                                                                                                                                                                                            AAR34545
888888888888888
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                                                                                                               E. coli as a fusion to the Pasteurella hamolytica leukotoxin gene lktA coded for by plasmid pAA352. The hmb gene fragment was taken from pRAP501 and starts at the codon for the third amino acid residue of ORF1. The hamin binding protein can be used in vaccines for preventing or treating H. Somnus infections, which cause thromboembolic meningo-encephalitis, septicaemia, arthritis and pneumonia in
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the same position on gels.

The LKT352 gene was prepd. as follows: lktA, an MaeI fragment contg. the gene was ligated into the SmaI site of pUC13 to form pAA179. From this, two constructs were made in the ptac-based vector, pGH432:lacI digested with SmaI. One, pAA342, consisted of the 5' AhaIII fragment from lktA while the other, pAA345, contained
                                                                                                       The hmb gene encoding the haemin-binding protein was expressed in
                                       Haemophilus somnus immunogenic proteins used in vaccines - selected from haemin-binding protein, haemolysin, LppB and LppC, and corresp. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKT352 is 98% homologous with authentic leukotoxin and migrates
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprise sub-unit antigens from P haemolytica fimbrial protein, plasmin receptor, 50 K outer membrane protein and leukotoxin.
                                                                                                                                                                                                                                                1.1%; Score 10; DB 14; Length 924; 00.0%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccines for Pasteurella haemolytica infection in cattle -
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawman MJP;
                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                       100.0%; Prea. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       AAR14482 standard; Protein; 926 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; leukotoxin; vaccine; lktA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bariuk LA, Potter AA,
                                                                                  Disclosure; Fig 5; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-CA00170
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry
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                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                           265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                  LAORVAAGLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pasteurella haemolytica
                                                                                                                                                                                            See also AAR42370-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-324967/44.
         WPI; 1993-351733/44
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                           924 AA;
                    N-PSDB; AAQ51081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1991;
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                                                                                                                                                                                   vertebrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acres SD,
                                                                                                                                                                                                                                                                                                                  256
                                                                                                                                                                                                                                                                                                                                                                                           AAR14482;
                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                         Matches
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in lambda gtil and pucil. Resulting clones were used to transform E. coli and individual colonies were pooled and screened for reaction with serum from a calf which had survived a P. haemolytica infection and that had been boosted with a conc. culture supernatant of P. haemolytica to increase anti-leukotoxin antibody levels. Positive colonies were screened for their ability to produce leukotoxin by incubating cell lysates with bovine neutrophils and measuring the release of lactate dehydrogenase from the neutrophils. A 4kb fragment was obtd. Progressively larger clones were isolated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
the entire Mael fragment. Clone pAA342 expressed a truncated leukotoxin peptide at high levels while pAA345 expressed full length leukotoxin at very low levels. The 3' end of the lkth gene of pAA345 was therefore ligated to Styl/BamHi digested pAA342 to yield pAA352 contg. the LKT352 sequence. The protein expressed from the vector can be used to prepare a subunit vaccine with other P. haemolytica antigens, e.g. fimbrial protein, plasmin receptor or 50K outer membrane protein. The vaccines can be used to protect cattle from respiratory diseases such as pneumonia, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene libraries of P. haemolytica Al (strain B122) were constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunological carrier system with enhanced immunogenicity - comprises chimeric protein comprising leuco:coxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12;
3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1%; SCC.
100.0%; Pred. No. J...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Redmond MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leukotoxin 352 produced from pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR34545 standard; Protein; 926 AA.
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AAW03945;
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                                                                                                         Sequence
                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                            AAW03945
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chromosome walking to isolate full length recombinants of ca. 8kb, in pAA114. The clone was subjected to restriction enzyme digestion to yield two clones, one expressing truncated leukotoxin peptide at high levels and the other expressing the full length leukotoxin at low levels. The 3' end of the lkth gene from the full length clone was ligated to the truncated gene clone to yield plasmid pAA352. The clone was used to produce chimeric proteins by gene fusion with an clone was used to produce chimeric proteins by gene foamtostatin, gonadotrophin releasing hormone or rotaving viral protein 4, i.e. leukotoxin works as a carrier protein to bring about a larger immune response than the antigen alone. Immunisation with these antigens can regulate growth rate, lactation and reproductive efficiency. See also AAR14546-8. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus somnus enriched with iron regulated proteins is new. The vaccine pref. further comprises an immunogenic leukotoxin polypeptide, esp. an immunogenic pasteurella haemolytica leukotoxin pomposous to LKT352. Example 1.2 describes the prodn. of P. haemolytica recombinant leukotoxin from pAA352. Two expression constructs were made. One, pAA342, contained the 5'-AhalI fragment of the ltkA gene, while the other, pAA345, contained the entire ltkA gene. PAA342 expressed a truncated leukotoxin peptide at high levels, while pAA345 expressed full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A vaccine comprising an outer membrane protein (OMP) extract of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; outer membrane protein; OMP; Haemophilus somnus; iron regulated protein; leukotoxin; Pasteurella haemolytica; LKT352.
                                                                                                                                                                                                                      1.1%; Score 10; DB 14; Length 926; 100.0%; Pred. No. 3.7; or Mismatches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus somnus outer membrane protein extract enriched with iron-regulated proteins, opt. contg. leuco:toxin antigens, for use as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant leukotoxin from plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pasteurella haemolytica Al (strain B122).
                                                                                                                                                                                                                                                                                                                                                                   AAR50291 standard; Protein; 926 AA.
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                                                                                                                                                                                                                                     Local Similarity 100.
Les 10; Conservative
                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                          265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-092909/12.
                                                                                                                                                                                                                                                                                                 256 LAORVAAGLS
                                                                                                                                                                                               926 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                     06-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA2099707-A.
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                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A truncated leukotoxin (AAW03945), LKT 352, lacks the cytotoxic portion of the native protein from Pasteurella haemolytica. It is the product of plasmid pAA352 which carries a truncated lktA gene (AAT37179). A fusion protein (AAW03942) between LKT352 and a gonadotropin releasing hormone terramer can be expressed in Escherichia coli. This is useful as a vaccine for fertility control, partic. immunological sterilisation of domestic or
length leukotoxin at very low levels. Therefore, the 3' end of the lktA gene was ligated into pAA342, yielding plasmid pAA352.
LKT352 or new leukotoxin is 98% homologous to authentic
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                                                                                                 NB: the protein sequence in Fig 5 comprises 926 amino acids, however this protein is described in the text as having 931 amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%; Score 10; DB 17; Length 926; 100.0%; Pred. No. 3.7; Arive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     DB 15; Length 926; 3.7;
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukotoxin; LKT; gonadotropin-releasing hormone; GRRH; fusion protein; immunogen; vaccine; fertility control; contraceptive; sterilisation; plasmid pAA352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P. haemolytica truncated leukotoxin (LKT352).
                                                                                                                                                                                                                                                                                   100.0%; Preα. ...
-ive 0; Mismatches
                                                                                                                                                                                                                                                                     1.1%; Score 10;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW03945 standard; Protein; 926 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifertility vaccine prodn.
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                                                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              265 LAQRVAAGLS 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-384447/38.
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                      926 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-NOV-1996
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                                                                                      leukotoxin.
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Leukotoxin; palktC; palktA; palktB; calcium dependent; RTX; cytotoxic protein; repeat of toxin; BL-3 cell; pig; lymphocyte; immunisation; diarrhoea; reagent;
                                                                                                                                                                                                                                                                                                                               /note= "glycine rich repeat sequence" 773..781
                                                                                                                                                                                                                                                                                                                                                       /note= "glycine rich repeat sequence"
                                                                                                                                                                                                                                                                                        /note= "glycine rich repeat sequence"
                                                                                                                                                                                                                                                                                                            /note= "glycine rich repeat sequence"
764..772
                    P. suis leukotoxin gene pslktA, protein product.
                                                                                                                                                                             /label= transmembrane_domain
710..718
/note= "glycine rich repeat 8
719..727
                                                                                                                                       'label= transmembrane_domain
                                                                                                                                                 295..311
/label= transmembrane_domain
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0972157.
94US-0215805.
                                                                        diagnosis; assay; enteritis
05-FEB-1997 (first entry)
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                                                                                                                                                                                                                          'note=
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                                                                                             Pasteurella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT45417
                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-NOV-1992;
22-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                             US5559008-A.
                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang Y;
                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a recombinantly produced or chemically synthesised leukotoxin 352 (LKT 352) polypeptide, derived from the lktA gene that is present in the plasmid pAA352. This gene produces a truncated protein that has an estimated molecular weight of about 99 kDa and lacks the cytotoxic portion of the molecule. Thus this gene has a higher expression level than that of the full-length molecule. This can be used in the construction of a chimeric protein that comprises a leukotoxin polypeptide, several multimers, and a GnRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
                                                                                                                                       Gonadotropin releasing hormone; GnHR; chimera; leukotoxin polypeptide; multimer; vaccine; tumour; Leukotoxin 352; LKT 352; lktA; plasmid pAA352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric protein of leukotoxin and gonadotropin releasing hormone -useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 19; Length 926; Pred. No. 3.7; 0; Mismatches 0; Indels
                                                                                                                                                                                                     Location/Qualifiers
11..924
/note= "Recombinant leukotoxin peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Figure 3.1-9; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW07637 standard; Protein; 934 AA.
                                                    AAW79568 standard; Protein; 926 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.1%; Scor
100.0%; Pred
0; M
                                                                                                                                                                                                                                                                                          97WO-CA00559
                                                                                                                                                                                                                                                                                                               96US-0694865
                                                                                                                    Leukotoxin 352 polypeptide
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                    (UYSA-) UNIV SASKATCHEWAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 LAORVAAGLS 265
 256 LAQRVAAGLS 265
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                                                                                                                                                                                                                                                                                                                                                          Potter AA;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-159540/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 LAQRVAAGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 AA;
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV61530.
                                                                                                                                                                                                                                                                                          08-AUG-1997;
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                                                                                               24-DEC-1998
                                                                                                                                                                                                                 Misc_feature
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                                                                                                                                                                                                                                                                      19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                          Manns JG,
                                                                                                                                                               cytotoxic.
                                                                                                                                                                                  Synthetic
                                                                        AAW79568;
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Best Local
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ID AAW0
XX AAW0
AC AAW0
XX 25-M
                               RESULT 2:
AAW79568
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"glycine rich repeat sequence"

"glycine rich repeat sequence"

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"glycine rich repeat sequence" "glycine rich repeat sequence"

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Leukotoxin genes from Pasteurella suis - also vectors and cells for expressing gene prods., for use in vaccines against porcine enteritis
                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is protein prod. of the Pasteurella suis leukotoxin gene pslkta, which together with the pslktc, and pslktb gene prods., comprises a high mol. wt. calcium dependent cytotoxic protein of the repeat of toxin family (RTX), capable of killing both BL-3 cells and pig lymphocytes. The leukotoxin proteins, and the pslktc, A and B genes, or fragments, can be used as immunogens in vaccines for the immunisation of pigs against diarrhoes, or as reagents in diagnostic assays. The leukotoxin genes were isolated by screening a P. suis genomic library, in the phage vector lambda-dash, with a DNA probe derived from PYFC19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carrying the IKtCA locus (Chang et al., Infect. Immun., Vol. 55, pp2248-2254, 1987).
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                                                                                                                                                                                                                                                                                                                              Claim 34; Columns 59-64; 47pp; English.
WPI; 1996-442408/44.
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Gaps

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Indels

RESULT 31

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AAR34547

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Oligonucleotides contg. sequences from bovine somatostatin (SRIF) gene were constructed on a Pharmacia Gene Assembler using standard phosporamidite chemistry. The oligonucleotides were annealed and ligated into vector pAA352 (contg. the Pateurella heamolytica leukotoxin gene) which had been digested with BamHi. The ligated DNA was used to transform E. coli strain JM105. Transformants contg. the oligonucleotide inserts were identified by restiction endonuclease mapping and the recombinant plasmid designated pAA496. The chimeric protein produced from the plasmid works to bring about a larger immune response than the antigen alone, i.e. the leukotoxin works as a carrier protein.

See also AAR34545-8.
(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                        Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
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1.1%; Score 10; DB 14; Length 943;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunological carrier system with enhanced immunogenicity comprises chimeric protein comprising leuco:coxin peptide homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..929
/note= "recombinant leukotoxin protein"
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            Mismatches
                                                                                                                                                                                                                                                                                                                          Somatostatin-leukotoxin gene fusion prod
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                                                                                                                                                                                     AAR34546 standard; Protein; 943 AA.
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(first entry)
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            10; Conservative
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                                                265 LAORVAAGLS 274
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256 LAQRVAAGLS 265
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23-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                             AAR34546;
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              Matches
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                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunological carrier system with enhanced immunogenicity - comprises chimeric protein comprising leuco:toxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
            DB 17; Length 934; 3.8;
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                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ______recombinant leukotoxin protein"
/note= "recombinant leukotoxin protein"
/note= "GnRH"
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100.0%; Pred. No. 3.8;
1.1%; Scc.
100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..926
                                                                                                                                                                                                                             AAR34547 standard; Protein; 936 AA.
                                                                                                                                                                                                                                                                                                                                                                GnRH-leukotoxin gene fusion prod.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92WO-CA00449.
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(first entry)
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            Query Match 1.1
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                        265 LAQRVAAGLS 274
                                                                                                                            279 LAORVAAGLS 288
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Best Local Similarity
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23-AUG-1993
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Protein Peptide

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256 LAQRVAAGLS 265
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                                                                                              AAR07167
                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                         Vector; LKT 352; flanking; recombinant; antigen; somatostatin; gonadotropin releasing hormone; rotavirus viral protein 4; carrier protein; lactation; reproduction; SRIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunological carrier system with enhanced immunogenicity - comprises chimeric proctein comprising leuco:coxin peptide or homologous protein fused to antigen esp. somatostatin or gonadotropin releasing hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "recombinant leukotoxin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                 Rotavirus VP4-leukotoxin gene fusion prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927..951
/note= "Rotavirus VP-4"
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                                                                                                                                                                AAR34548 standard; Protein; 951 AA
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(first entry)
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265 LAQRVAAGLS 274
                                          256 LAQRVAAGLS 265
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23-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                AAR34548;
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Protein
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                                                                                                                    RESULT 33
                                                                                                                                          Solution of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of th
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Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine against shipping fever in cattle - contains purified Pasteurella haemolytica antigen of molecular wt. 105 kD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 10; DB 11; Length 953;
100.0%; Pred. No. 3.8;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Weinstock G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella haemolytica Al (ATCC 43270)
                                                                                                                                                                                                                                                                                                                                                                                               Berget P, Engler M, Highlander S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 9a-h; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR15159 standard; Protein; 953 AA.
AAR07167 standard; protein; 953 AA.
                                                                                                      105kD PTX protein of P.haemolytica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukotoxin from P. haemolytica.
                                                                                                                                                                                                                                                                                     87US-0085430.
                                                                                                                                                                                                                                                                                                                          87US-0085430.
                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV OF TEXAS SYSTE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JAN-1992 (first entry)
                                                                  24-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                         Vaccine, shipping fever.
                                                                                                                                                                           Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 LAQRVAAGLS 292
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-304558/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 953 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ06074
                                                                                                                                                                                                                                                                                       13-AUG-1987;
                                                                                                                                                                                                                                                                                                                          13-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-1986;
                                                                                                                                                                                                                US4957739-A.
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265 LAQRVAAGLS 274

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This protein is a 105 kD antigen which may be used in vaccines to protect cattle against shipping fever. The antigen is also useful for raising antisera which can be used for passive immunisation (for treatment or temporary prophylaxis) and also to raise antibodies which can be used in immunoassay methods for the detection of Pasteurella haemolytica antigens in biological fluids. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica; shipping fever; pasteurellosis; cattle; vaccine; treatment; therapy; prophylaxis; antigen; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified antigen from Pasteurella haemolytica - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccines against shipping fever of cattle, also for raising antibodies useful in diagnosis and passive immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%; Score 10; DB 15; Length 953;
100.0%; Pred. No. 3.8;
cive 0; Mismatches 0; Indels
                                                                                                   Length 953;
culture supernatant derived from a culture of Pasteurella
                                                                                                                                       Indels
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                    DB 14;
3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weinstock
                   haemolytica.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                 PtxA protein of Pasteurella haemolytica.
                                                                                                    1.1%; Score 10;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Highlander S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Figure 9; 35pp; English.
                                                                                                                                                                                                                                                                                              AAR60072 standard; Protein; 953 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-0935806.
87US-0085430.
90US-0540261.
92US-0899100.
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                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                              11|||||||
283 LAQRVAAGLS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella haemolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274
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                                                                                                                                                                         265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berget P, Engler M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-255245/31.
N-PSDB; AAQ70050.
                                                                                                                      Local Similarity
nes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  953 AA;
                                                                      953 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987;
18-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
13-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5336491-A.
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                                                                                                                                                                                                                                                                                                                              AAR60072;
                                                                      Sequence
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                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                        Matches
                                                                                                                                                                                                                                                            RESULT 37
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                                                                                                                                                                                                                                                                            AAR60073
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0
                                                                                                                                                                                                                                        ORF2 (AAR14223) codes for a 19.820 D protein of 166 amino acids; ORF1 codes for leukotoxin, a 101.883 D protein of 952 amino acids, which is produced on expression of pLKT5 in a host organism. The leukotoxin has cytotoxic activity specific against leukocytes. The protein is used to prepare vaccines or to raise antibodies against P. haemolytica to protect cattle from pneumonic pasteurellosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic determinants; peptides; vaccine; supernatant; leukotoxin.
                                                                                                                                       DNA encoding Pasteurella haemolytica-Al leukotoxin - used to produce recombinant protein for prepn. of vaccine and antibodies for protection of cattle from pneumonic pasteurellosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One or more biologically pure antigenic determinants of the leukotoxin protein comprising of at least six amino acids is a component of a new vaccine for animals. The vaccine elicits an enhanced immune response after challenge with Pasteurella haemolytica. The vaccines other component is a bacterial free
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                   1.1%; Score 10; DB 12; Length 953; 100.0%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine for preventing Pasteurella haemolytica infections contains leukotoxin protein antigenic determinants and P. haemolytica culture supernatant
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strathdee CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR43865 standard; Protein; 953 AA.
                                                      Strathdee CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Figure 1; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shewen PE,
                                                                                                                                                                                                           Claim 6; Page 15; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92CA-2081950
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pasteurella haemolytica
                   (UYGU-) UNIV OF GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||||||||
LAQRVAAGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conlon JA, Lo RYC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-227822/29.
                                                      Shewen PE,
                                                                                      WPI; 1991-317648/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYGU-) UNIV GUELPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukotoxin protein.
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  953 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ46410
                                                                                                      N-PSDB; AAQ14000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
22-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
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                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                      Lo RYC,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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AAR43865
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AAE04638;

RESULT 38 AAE0463 Domain Domain Domain

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A chimeric protein (AAW03942) is composed of a fusion between a truncated leukotoxin (LKT-352) from Pasteurella haemolytica (see also AAW03945) and a 4-copy gonadoliberin-releasing hormone (GnRH) repeat sequence (see also AAW03944). It is the product of a chimeric gene (AAT37176) produced by ligating a synthetic sequence for the 4-copy GnRH into vector PAA52 (ArCC 68283), which carries the LKT-352 gene. Recombinant plasmid pCBH13 (LKT 352.4 copy produced the chimeric protein, which is useful as a vaccine for demestic or farm animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gonadotropin-releasing hormone multimer fusion proteins - with leukotoxin polypeptide for increased immunogenicity, useful in antifertility vaccine prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 10; DB 17; Length 977;
100.0%; Pred. No. 3.9;
tive 0; Mismatches 0; Indels
                                                                                                            Leukotoxin, LKT, gonadotropin-releasing hormone, GnRH, fusion protein; immunogen; vaccine; fertility control; contraceptive; sterilisation.
                                                                                                                                                                                    Chimeric Pasteurella haemolytica Al strain B122;
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                      927..977
/label= GnRH_repeat_domain
                                                                          LKT-GnRH protein fusion from pCB113.
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW79569 standard; Protein; 977 AA
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                                                                                                                                                                                                                                                                                    /label= LKT
                                    20-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1998 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               265 LAORVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potter AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-384447/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         977 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT37176.
                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                WO9624675-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manns JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
AAW03942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW79569;
                                                                                                                                                                                                                                                  Key
Domain
                                                                                                                                                                                                                                                                                                          Domain
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ID AAW7
XX
AC AAW7
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DT 24-E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is Pasteurella (Mannheimia) haemolytica full length leukotoxin protein. The present invention relates to modified leukotoxin DNA sequences, wherein the modification comprises the removal of DNA sequence encoding the amino acids within the hydrophobic transmembrane domain of a full length leukotoxin protein. Modified leukotoxin sequences are used in vaccines to treat or prevent diseases associated with leukotoxin, e.g., respiratory disease, and Mannheimia infection (particularly M. haemolytica infection). In addition, the vaccine is used to prepare a medicament. Purthermore, the plant transformed with modified leukotoxin sequences is fed to an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified leukotoxin polypeptide is useful in a vaccine to prevent or treat Mannheimia (Pasteurella) infection (particularly M. haemolytica infection), and disease associated with a leukotoxin, e.g., respiratory
                                                                                                                                                                                                                            Leukotoxin; respiratory disease; infection; therapy; immunostimulant; antibacterial; vaccine; transgenic plant; animal feed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       such as a ruminant, to prevent or treat respiratory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1%; Score 10; DB 22; Length 953;
100.0%; Pred. No. 3.8;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                280..320
/label= Hydrophobic_transmembrane_domain_2
360..400
/label= Hydrophobic_transmembrane_domain_3
                                                                                                                                                                                                                                                                                                                                                            /label= Hydrophobic_transmembrane_domain_l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hodgins D, Strommer JN,
                                                                                                                                                                                        Pasteurella haemolytica leukotoxin protein.
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                        AAE04638 standard; Protein; 953 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 13; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee RWH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-2000; 2000WO-CA01498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0172148
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                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                      Pasteurella haemolytica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewen PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-408470/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200144289-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1999;
                                                                                                                                                    10-SEP-2001
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Lo RYC,

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Gaps

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LKT-GnRH chimeric protein.

AAW03942 standard; Protein; 977 AA.

RESULT 39
AAW03942
ID AAW035

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Sequence

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The present sequence represents the LKT-GRRH chimeric protein from pCB113. This plasmid contains the LKT 352 polypeptide (AAW79568) fused to four copies of the GRRH peptide. This chimera lacks cytocoxic activity which enables there to be an increase in antigen presentation and thus an optimal immune response. The removal of this region also enables the truncated LKT to be expressed at much higher levels and allows the amount of antigen administered to be reduced. This chimeric protein comprises a leukotoxin polypeptide, several multimers, and a GRRH sequence. The chimeric protein can be used as a vaccine to help reduce the incidence of mammary tumours in a mammalian individual.
Chimera; pCB113; LKT 352; GnRH; Gonadotropin releasing hormone; multimer; cytotoxic activity; antigen presentation; immune response; vaccine; tumour.
                                                                                                                                                                                                                                                                                                                                                                                        Chimeric protein of leukotoxin and gonadotropin releasing hormone -useful for, e.g. preparation of vaccines for reduction of incidence of mammary tumours in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1%; Score 10; DB 19; Length 977; 100.0%; Pred. No. 3.9; tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 10; Conservative
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N-PSDB; AAV61531.
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                                                                            Synthetic.
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Search completed: February 17, 2004, 10:19:35 Job time : 66 secs

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Gaps

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GenCore version 5.1.6
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PRINTS; PRO0313; CABNDNGRPT.
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PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
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InterPro; IPR003995; RtxA.
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Pfam; PF02382; RTX; 1.
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Pasteurellaceae; Mannheimia.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
PROSIMEM 229 249.
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D -> Y (IN REF. 2).
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7F93D113A118C05F CRC64;
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              EMBL; M20730; AAA25529.1; -.
EMBL; M34197; AAA25543.1; -.
PIR; B30169; B30169; B30169; Increro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
                                                                                                                 Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
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GTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSYTVNRFVETGKALHEVTSTHTAL 681
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                                                                VGKRTETIQYRDYELRKVGYGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDL
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MEDLINE=94041617; PubMed=8225575;
Burrows L.L., Olah-Minfield B., Lo R.Y.C.;
Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly DEFINED.
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DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
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--- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).
--- PTM: Palmitoylated by lktC. The toxin only becomes active when modified (By similarity).
--- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leukotoxin from serotype All.
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                         tch 50.2%; Score 2332; DB 1; Length 953; al Similarity 49.1%; Pred. No. 7.1e-110; 467; Conservative 183; Mismatches 261; Indels 40
Repeat; Calcium; Transmembrane,
                                                                                                                                                                                            102206 MW; 927PFS6CFC884F12 CRC64;
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6 X REPEATS, GLY-RICH
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   Cytolysis;
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                Lipoprotein;
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                                                                         PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSXITSDQIDKILQDKKDGTVITSQELK 871
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-!- FUNCTION: Virulence factor which is cytotoxic for leukocytes but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93239320; PubMed-8478098;
Chang Y.-F., Ma D.-P., Shi J., Chengappa M.M.;
"Molecular characterization of a leukotoxin gene from a Pasteurella
haemolytica-like organism, encoding a new member of the RTX toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not hemolytic.
--- SUBCELLIAR LOCATION: Secreted.
--- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
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-!- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).
-!- PTM: Palmitoylated by thtC. The toxin only becomes active when modified (By similarity).
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasteurella haemolytica-like sp. (strain 5943B).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaces; Pasteurella.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
Hemolysis; TOXAL; CYtolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
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34, Last sequence update)
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InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
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947 AA;
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TRANSMEM 1
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                        16;
                                                                         AADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKG 106
                                                                                   107 LDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEII 166
                                                                                                                    PGSSENVAKNLGNAQTLLSGIQSILGSVWAGMDLDEILKNKGSELD-LAKAGLELTNSLI 179
                                                                                                                                                      299
                                                                                                                                                                                                              SIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTIS 345
                                                                                                                                                                                                                     TALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEW 405
                                                                                                                                                                                                                                                        360 TALAAISGGVSAAAAGSLVGAPIALLVSGITGIISTILQYSKQAMFEHVANKIHDKIVDM 419
                                                                                                                                                                                                                                                                                EKONGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGIT 465
                                                                                                                                                                                                                                                                                         EKKHNGKNYFENGYDSRYLADLQDNMRQLQNLNKELQAERVIRITQQQWDNNIGNLAGIS 479
                                                                                                                                                                                                                                                                                                                KLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAG 525
                                                                                                                                                                                                                                                                                                                                539
                                                                                                                                                                                                                                                                                                                                                 TESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA-----ETEGTD 578
                                                                                                                                                                                                                                                                                                                                                                                 EIGLIVNAKAGNDDIFVGOGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVN 638
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                                                                                                                                           GNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLONLN-FSKTNLGLEIITGLLSGI
                                                                                                                                                                            SAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLA
                        Gaps
                        40;
        Length 947;
       Query Match 49.6%; Score 2306; DB 1; Length 9. Best Local Similarity 50.0%; Pred. No. 1.4e-108; Matches 466; Conservative 173; Mismatches 253; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DENKSQKLSASDIAS-SLNKLVGSMALFGTAN 905
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953 AA.

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STANDARD;

RESULT 4 LKA3_PASHA ID _LKA3_PASHA

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                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity.
--- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).
--- PIM: Palmitoylated by lktC. The toxin only becomes active when modified (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                             Pasteurella haemolytica.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
48.5%; Score 2256; DB 1; Length 9
Best Local Similarity 48.7%; Pred. No. 4.6e-106;
Matches 463; Conservative 174; Mismatches 270; Indels
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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POTENTIAL.
POTENTIAL.
6 X REPEATS, G
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Interpro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PP02382; RTX; 1.
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                                                                           Leukotoxin from serotype T3.
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TRANSMEM 22
TRANSMEM 29
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                                                                                                                                                                                                                                                                                                                                                          "Cytolysins of Actinobacillus pleuropneumoniae serotype 9.";
Infect. Immun. 59:4497-4504(1991).
Infect. Immun. 59:4497-4504(1991).
Infect. Immun. 59:4497-4504(1991).
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STRAIN=Serotype 5;
MEDLINE=90126233; PubMed=2693022;
Chang Y.-F., Young R., Struck D.K.;
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DNA 8:635-647(1989).
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Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
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STRAIN=Isolate CVI 13261 / Serotype 9;
STRAIN=S2040145; PubMed=1937809;
Smits M.A., Briaire J., Jansen R., Smith Gielkens A.L.;
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EMBL; X6111; CAA43423.1; -.
PIN; B33389; B33389; B3389; InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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                                                                                                                                                                     53; Gaps
                                                                                                                                     Query Match 48.1%; Score 2236.5; DB 1; Length 956; Best Local Similarity 47.7%; Pred. No. 4.4e-105; Matches 453; Conservative 188; Mismatches 255; Indels 53;
                                                                                                               BDBCABBADF14A641 CRC64;
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RTX-II toxin determinant A (APX-IIA) (Hemolysin IIA) (HLY-IIA)
(Cytolysin IIA) (CLY-IIA).
APXIIA OR CLYIIA OR HLYIIA OR APPA OR CYTC.

HT2A_ACTPL 1D RT2A_A AC P15377 DT 01-APR DT 28-PEB DE (Cytol GN APXIIA GN APXIIA GN APXIIA GN APXIIA CO Pasteu OC Pasteu OC Pasteu RP 11]

956 AA

STANDARD;

RT2A ACTPL P15377;

Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae) Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Actinobacillus. NCBI_TaxID=715;

SEQUENCE FROM N.A

GLY-RICH

X REPEATS,

POTENTIAL. POTENTIAL. POTENTIAL

S.

FUNCTION: Bacterial hemolysins are exotoxins that attack blood call membranes and cause cell rupture by mechanisms not clearly

defined

SUBCELLULAR LOCATION: Secreted. DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic

activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).

PTM: Palmitoylated by lktC. The toxin only becomes active when MODIFIED (BY SIMILARITY).

SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.

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Lainson F.A., Murray J., Davies R.C., Donachie W.;
"Characterization of epitopes involved in the neutralization of Pasteurella haemolytica escrotype Al leukotoxin.";
Microbiology 143:2499-2507(1996).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blo
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PRINTS; PR00133; CABNINGRPT.
PROSITE; PS01330; HEMOLYSIN CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Tripoprotein; Palmitate.
POTENTIAL.
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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    KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK
                   ASIDLINEIIGNLSOSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGL
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                                                                                                                                                                                                                                                         169 LSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISA
                                                                                                                                                                                                                                                                                                            5 NVIKSNIQA---GLN-----STKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAA
                                                                                                                                                                NGIRSTLTATRGGLNRAGQSLTQAGQTLKNGAKKIILYIPKDYKYDSGSGNGLQDLVKAA
                                                                                                                                                                                          DELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLD
                                                                                                              Gaps
                                                                                                               44;
                                                                                    Length 955;
                                                                                   48.1%; Score 2236; DB 1; Length 9
48.2%; Pred. No. 4.7e-105;
ive 178; Mismatches 271; Indels
                                                              CRC64;
                                                              B60F2DB8168EBCAF
                                                                                    Query Match
Best Local Similarity 48.2%; Pre
Matches 458; Conservative 178;
                                                              102187 MW;
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955 AA;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Mannheimia.

Pasteurella haemolytica.

SEQUENCE FROM N.A. STRAIN=Serotype T10; NCBI_TaxID=75985;

01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leukotoxin from serotype T10.

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STANDARD;

PASHA

LKAA PA P55117;

GLY-RICH

POTENTIAL.
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                                                                                                                                              GLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRK 640
                                                                                                                                                      VARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVF 700
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                                                                                                                                                                                                                 DVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY- 819
                                                                                                                                                                                                                                            LGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEK 407
                                   ---ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADE 876
                                                                                                                                                                                                                                                                         EAEFAKTIQNYVATR-DDKIEEIIGGNGERITSKQVDELIE--KGNGKIAGSELTKVVDN 901
                                                                                                                                                                                   MLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLTTISTA
                                                                                             QNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKL
                                                                                    GERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTE
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                                                                                                                                                                                                                                                                                              NKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAPSV 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity.
DOMAIN: The three transmembrane domains are believed to be
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hemolysin (Cytolysin II) (CLY-IIA) (HLY-IIA) (CYTC) (APPA)
APPA OR CLYIIA OR HLYIIA OR CYTC.
Actinobacillus suis.
                                                                                                                                                                                                                                                                                                                                                956 AA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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involved in pore formation by the cytotoxin (By similarity PYM: Palmitoylated by lktC. The toxin only becomes active modified (By similarity). Similarity: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0313; CABNUNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSTITE; P800330; HEMOLYSIN CALCIUM, 1.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 2214.5; DB 1; Length ilarity 47.4%; Pred. No. 5.6e-104; Conservative 188; Mismatches 258; Indels
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InterPro, IPR001343; Hemlysn_Ca_bind
InterPro, IPR003995; RtxA.
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00353; hemolysinCabind; 5. Pfam; PF02382; RTX; 1.
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Palmitoylated by apxIIIC. The toxin only becomes active when

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                                                                                                                                                                                                                                                                                                                                                     771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKD 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             887
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X MEDLINE-93162836; PubMed=8432615;

MEDLINE-93162836; PubMed=8432615;

Annean R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;

T "Cloning and characterization of the Actinobacillus

T pleuropneumoniae-RTX-toxin III (ApxIII) gene.";

Infect. Immun. 61:947-954(1993).

-1- FUNCTION: Does not have hemolytic activity but shows a strong cytotoxicity towards alveolar macrophages and neutrophils.

-1- FUNCTION: Does not have hemolytic activity but shows a strong cytotoxicity towards alveolar macrophages and neutrophils.

-1- FUNCTION: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic activity (By similarity).

-1- DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).
                      NOIGDLAAISRRTDKISSGKAYVDAFEEGNTSPSIHPYSIDNKNGIINISNTN-RKTQSV
                                                                                                 DDAGNIIESKDTK---IIANLGAGNDNVFVGSSTTVIDGGDGHDRVHYSR-GEYGALVID
                                                                                                                                                                                                                                                                                                                                    KSVEEIIGSQFNDIFKGSQFDDVFHGGNGVDTIDGNDGDDHLFGGAGDDVIDGGNGNNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          831 INQKGEKVRIGNWFLEDDLASTVANYKAT-NDRKIEEIIGKGGERITSEQVDKLI--KEG
NNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQAL
                                                                                                                                                        ----ETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVD
                                                                                                                                                                                                                                   GTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNL
                                                                                                                                                                                                                                                             KSVEEVIGSOFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: characterization of the ApxIII operons."; Infect. Immun. 62:4411-4418(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jansen R., Briaire J., van Geel A.B.M., Kamp E.M., Gielkens A.L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 41, Last annotation update)
RTX-III toxin determinant A from serotype 8 (APX-IIIA) (Cytolysin IIIA) (CY-IIIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSN 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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MEDLINE=95012630; PubMed=7927703;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 TISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
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PRINTS; PRO1488; RTXTOXINA.
PROSTIE; PS00330; HEMOLYSIN CALCIUM; 3.
TOXID; Cytolygie; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
         modified (By similarity).
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      112809 MW; F83AFE25A6FD8758 CRC64;
                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
7 X REPEATS, GLY-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.1%; Score 1955.5; DB 1; llarity 42.6%; Pred. No. 6.6e-91; Conservative 166; Mismatches 287;
                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                           EMBL, X68815, CAA48711.1; -.
PIR, B49219, B49219.
InterPro, IPR001343; Hemlysn_Ca_bind.
                                                                                                                                                                                     Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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                                                                                                                                  EMBL; X80055; CAAS6358.1; -.
                                                                                                                                                                            InterPro; IPR003995; RtxA
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1052 AA;
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                                            EAGSYTVNRKVARG-DIYHEVVKRQETKVGKRTETIQYRDYELRKVG-YGYQSTDNLKSV 688
                                                                                                                                                                                         LNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVKRNDHS 810
                                                                                                                                                                                                                                                                                          ---GSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS 867
                                                                                                                                                                                                                                                                                                       912 HNNGVLTIKDWF-----KEGNKYNHKIEQIVDKNGRKLTAENLGTYFKNAPKADNLLN 964
LEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQORWDNNIGELA 462
                                                                                                                                                                                                                   DLLDGGSGDDV 753
                                                                                                                                                                                                                                    792 EGNDKLIGGNGNNYLSGGDGNDELQVIGNGFNVLRGGKGDDKLYGSSGSDLLDGGEGNDY 851
                                                                                                                                                      SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDG--EASSKLDFSKVIQR----
                                                                                                         VAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSAT
                                                                                                                                                                                EEVIGSQFNDVFKGSKFND1FHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Appoperons: characterization of the ApxIII operons.";
Infect. Immun. 62:4411-4418(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                      RTX-III toxin determinant A from serotype 2 (APX-IIIA) (Cytolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRANIE-SEVOTYPE 2;
MEDLINE-9326392;
Chang Y.-F., Shi J., Ma D.-P., Shin S.J., Lein D.H.;
Chang Y.-F., Shi J., Ma D.-P., Shin S.J., Lein D.H.;
"Molecular analysis of the Actinobacillus pleuropneumoniae RTX
toxin-III gene cluster.";
DNA Cell Biol. 12:351-362 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jansen R., Briaire J., van Geel A.B.M., Kamp E.M.,
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                                                                                                                                                                                                                                                                                                                              QELKKLADENKSQKLSASDIASSLNKLVGSMALFGTA
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            1049 AA
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MEDLINE=95012630; PubMed=7927703;
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APXIIIA OR CLYIIIA OR RTXA OR
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28-FEB-2003 (Rel
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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PRINTS; PR01488; RTXTOXINA.
PROSTITE; PS00330; HEMOLYSIN CALCIUM; 3.
TOXIN; CYLOJYSis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
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POTENTIAL.
11 X REPEATS, GLY-RICH
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43.0%; Pred. No. 2.5e-89;
ive 152; Mismatches 296;
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InterPro; IPR001343; Hemlyen_Ca_bind.
InterPro; IPR003995; RtxA.
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EMBL; X80056; CAB37652.1; ALT_SEQ.
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Matches 428; Conservative
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                                                                                                             LEWEKONGGONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELA
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Hess J., Wels W., Vogel M., Goebel W.; "Nucleotide sequence of a plasmid-encoded hemolysin determinant and its comparison with a corresponding chromosomal hemolysin sequence.";
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MEDLINE=95099325; PubMed=7801126;
Stanley P., Packman L.C., Koxonakis V., Hughes C.;
"Fatry acylation of two internal lysine residues required for the
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Plasmid Incl2 pHIX152.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Last annotation update)
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                                                                                                01-JAN-1988 (Rel. 06, 01-JAN-1988 (Rel. 06, 28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                    Hemolysin, plasmid.
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22; 67

Gaps

Indels 117; DB 1; Length 1024;

8 KSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAK

Matches 418; Conservative 156; Mismatches 312;

41.78;

Similarity

Query Match Local

8

39.8%; Score 1848.5; DB 41.7%; Pred. No. 1.5e-85;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANBOUS: The hemolysin of E.Coli is produced predominantly by strains causing extraintestinal infections, such as those of the urinary tract.

SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                  J. Bacteriol. 178:5422-5430(1996).
-!- FUNCTION: Bacterial hemolysins are exotoxins that attack blood
cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                          -!- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      involved in pore formation by the cytotoxin.
-!- PTM: Palmitoylated by hlyC. The toxin only becomes active when modified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity.
DOWAIN: The three transmembrane domains are believed to be
                                                                                                                                          R., Hoppe J.,
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PRINTS; PR01488; RIXYOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 4.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitare; Plasmid.
                                                                                                                                                                                           "Analysis of the in vivo activation of hemolysin (HlyA) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110201 MW; 83944917F76C945B CRC64;
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                                                                                                                                          Benz
toxic activity of Escherichia coli hemolysin."; Science 266:1992-1996(1994).
                                                                             PALMITOYLATION OF LYS-564 AND LYS-690.
MEDLINE=96404790; PubMed=8808931;
Ludwig A., Garcia F., Bauer S., Jarchau T.,
Goebel W.;
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Pfam; PF02382; RTX; 1.
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362 IDDDGGKEDKLSLADIDFRDVAFKREGNDLIMYKGEGNVLSIGHKNGITFRNWF----E
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                                                                                                                                                                      Felmlee T., Pellett S., Welch R.A.; "Nucleotide sequence of an Escherichia coli chromosomal hemolysin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: The hemolysin of E.coli is produced predominantly by strains causing extraintestinal infections, such as those of
                                                                                                                                                                                                                                                                                                                                                                  defined.
SUBCELLULAR LOCATION: Secreted.
DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                   STRNIN=2001;
MEDLINE=68258115; PubMed=3894051;
Micaud J.-M., Mackman N., Gray L., Holland I.B.;
"Characterisation of Hlyc and mechanism of activation and secretion
                                                                                                                                                                                                                                                                                                                                     FUNCTION: Bacterial hemolygins are exotoxins that attack blood cell membranes and cause cell rupture by mechanisms not clearly
                                                                                                                                                                                                                                                                                                                                                                                                                                                        involved in pore formation by the cytotoxin. PTM: Palmitoylated by hlyC. The toxin only becomes active when modified.
                                                       Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                             activity.

DOMAIN: The three transmembrane domains are believed to be
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Pfam; PF02382; RTX; 1.
PRINTS; PR00313; CABNINGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the urinary tract. SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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POTENTIAL.
16 X REPEATS, GLY-RICH.
Last sequence update)
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PIR; A24433; LEECA.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001395; RtxA.
                                                                                                                                                                                                                                                                                                       haemolysin from E. coli 2001.";
S Lett. 187:339-344(1985).
                                                                                                                                            STRAIN=J96 / Serotype O4;
MEDLINE=85234404; Pubmed=3891743;
                                                                                                                                                                                                      Bacteriol. 163:94-105(1985)
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(Rel. 10, (Rel. 41,
                             Hemolysin, chromosomal
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01-MAR-1989
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                                                                                                                 Gaps
                                                                                                39.7%; Score 1845; DB 1; Length 1023;
.larity 41.8%; Pred. No. 2.2e-85;
Conservative 156; Mismatches 311; Indels 118;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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861 IDDDGGKDDKLSLADIDFRDVAFRREGNDLIMYKAEGNVLSIGHKNGITFKNWF----E
                                                                                                                                                   916 KESGDISNHQIEQIFDKDGRVITPDSLKKALEYQQSNNKASYVYGNDALAYGSQGNLNPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Hemolysin IA)
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-!-DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).
-!- PTM: PALMITOYLATED BY APXIC. The toxin only becomes active when modified (By similarity).
-!- MISCELLANEOUS: APXIA is partially deleted in serotypes 2, 4, 6, 8, 12, and totally deleted in serotype 3.
-!- MISCELLANEOUS: The sequence shown is that of serotype 10.
-!- SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=13039 / Serotype 10;
MEDLINE=94276858; PubMed=8007819;
Nagai S., Yagihashi T., Ishihama A.;
"DNA sequence analysis of an allelic variant of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxIA) from serotype 10.";
Microb. Pathog. 15:485-495(1993).
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Infect. Immun. 61:3688-3695(1993).
-!- FUNCTION: One of the virulence factors of A.pleuropneumoniae,
which has a strong hemolytic activity and is cytotoxic for
alveolar macrophages and neutrophils.
                                                                             DGTVITSQ-
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                                                                   STRAIN=K17 / Serotype 5;
MEDLINE=96401417; PubMed=8807793;
Chin N., Frey J., Chang C.F., Chang Y.F.;
"Identification of a locus involved in the utilization of
                                                                                                                                                                                                                            --ELKKLADENKSQKLSASDIASSLNKLVGSMALFGTA-NSVSSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APX-IA)
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01-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RTX-I toxin determinant A from serotypes 5/10
APXIA (CYtolysin IA) (CLY-IA).
                                                                         NYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKK-
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FEMS Microbiol. Lett. 143:1-6(1996)
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SEQUENCE OF 886-1023 FROM N.A.
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611 HLGEKNDRIYLSSGSSIVYAGNGHDVAYYDKTDTGY--LTFDGQSAQKAGEYIVTKELKA 668
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STRAIN=Isolate CVI 13261 / Serotype 9;
MEDLINE=9336642; PubMed=8359891;
Jansen R., Briaire J., Kamp E.M., Gielkens A.L.J., Smits M.A.;
"Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI) operon.";
DDLLDGGSGDD------VLNGGAGNDVY-----IFRKGDGNDTLYDGTGND---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNA
                                                                                                                                                                       KAG--NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
RTX-1 toxin determinant A from serotypes 1/9 (APX-IA) (Hemolys: (HLY-IA) (Cytolysin IA) (CLY-IA).
APXIA OR CLYIA OR HLYIA.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
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MEDLINE=94237497; PubMed=8181764;
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STRAIN=S 4074 / Serotype 1;
MEDLINE=91348845; PubMed=1879928;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 ASNVLSTLSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 IEAFSSQLAKLGS---TISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNKDADAGTKAAAGIEISTKILGNIGKAVSQYIIAQRVAAGLSTTAATGGLIGSVVALAI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPLSFLNVADKFERAKQLEQYSERFKKFGYEGDSLLASFYRETGALEAALTTINSVLSAA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERI 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTE 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSNIQAGLNSTKSGL-----KNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
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37.2%; Score 27.2.1.4e-79;
Best Local Similarity 39.5%; Pred. No. 1.4e-79;
Matches 403; Conservative 177; Mismatches 312; Indels
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E -> Q (IN REF. 2).
TC -> R (IN REF. 2).
F -> L (IN REF. 2).
Mw; 183C7C15EE57DB55 CI
                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
POTENTIAL.
13 X REPEATS, GLY-RICH
EMBL; D16582; BAA04014.1; -.
EMBL; 104594; ABA17220.1; -.
EMBL; X73116; CAA51546.1; -.
PIR; I39641; I39641.
InterPro; IPR001343; Hemlyan_Ca_bind.
InterPro; IPR001343; Hemlyan_Ca_bind.
InterPro; IPR00395; RtxA.
Pfam; PF00353; hemolyainCabind; 6.
Pfam; PF00313; CABNOGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00313; CABNOGRPT.
Hemolyais; Toxin; Cyclyysis; Repeat; Calcium; Trailpoprotein; Palmitate.
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TRANSMEM 22
TRANSMEM 29
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                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                  7
                      SEQUENCE FROM N.A.
STRAINES 4014 / Serotype 1;
Chang Y., Wang Y., Chin N.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: One of the virtulence factors of A.pleuropneumoniae,
which has a strong hemolytic activity and is cytotoxic for
alveolar macrophages and neutrophils.
-!- SUBCELLIARA LOCATION: Secreted.
-!- SUBCELLIARA LOCATION: Secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                         activity.
DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (By similarity).
PTM: Palmitoylated by apxIC. The toxin only becomes active when
                                                                                                                                                                                     modified (By similarity).

MISCELLANEOUS: ApxIA is partially deleted in serotypes 2, 4, 8, 12, and totally deleted in serotype 3.

MISCELLANEOUS: The sequence shown is that of serotype 1.
SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.1%; Score 1723; DB 1; Length 1023; 39.7%; Pred. No. 3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 2.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYLTLA -> GNALSNTR (IN REF. -> A (IN REF. 3 AND 4). -> E (IN REF. 3 AND 4). -> E (IN REF. 3 AND 4).
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12.
13.
AMPYLTLA -
R -> A (IN
Q -> E (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                            EMBL; X73117; CAA51548.1; -.
EMBL; U05042; AAB05034.1; -.
PIR, 139643; I19643; I19643.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001395; RtxA.
Pfem; PF00353; RTXA.
Pfem; PF00353; RTX; I.
Infect. Immun. 61:3688-3695(1993)
                                                                                                                                                                                                                                                                                                                                                     EMBL; X52899; CAA37081.1; -. EMBL; X68595; CAA48586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1023 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein;
TRANSMEM 2
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                                              119
                                                                                                                                                                  SNKDADAGTKAAAGIEISTKILGNIGKAVSQYIIAQRVAAGLSTTAATGGLIGSVVALAI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAGVGAAATGSLVGAPVAALVSAITGIISGILDASKQAIFERVATKLANKIDEWEKKH-G 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERI 471
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                                                                                                                                                                                                                                     176 IEAFSSOLAKIGS---TISQAKGFŞNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFAL 231
                                                                                                                                                                                                                                                              SPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
                                                                                                                                                                                                                                                                                                                                   232 ADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAI 291
  80
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                                              NHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL-DSVENIDRKLGK
                                                                                                                                       .20 ASNVLSTLSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSGKAYADAFEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587 KAG--NDDIFVGQGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKV-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 RGDIYHEVVKRQETKVGKR-TETIQYRDYELR--KVGYGYQSTDNLKSVEEVIGSQFNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 FFGSRFTDIFHGAKGDDEIYGNDGHDILYGDDGNDVIHGGDGNDHLVGGNGNDRLIGGKG
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21 KSAAKSGAGALKNGLGQVKQAGQKLILYIPKDYQASTGSSLNDLVKAAEALGIEVHRSEK
                                                                                        81 NGTALAKELFGTTEKLLGFSERGIALFAPQFDKLLNKN--OKLSKSLGGSSEALGQRLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------BLLDGGAGDDRLFGGKGNDRLSGDEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    874 ADENKSQKLSASDIASSLNKLVGSMALF-GTANSVSSNALQPI 915
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LKTA_ACTAC
ID LKTA_ACTAC
AC 116462;
DT 01-AUG-1990 (
DT 01-AUG-1990 (
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28; 9

Gaps

309; Indels 116;

180; Mismatches

Conservative

Local Similarity les 398, Conserv

Best Loca Matches

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Indels

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Conservative 167; Mismatches 292;
391;
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                                                                                                                                                             177
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                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                            Biol. Chem. 264:15451-15456(1989).
FUNCTION: One of the virulence factors of A.actinomycetemcomitans might be a cytotoxin, possibly the membrane-bound hemolysin.
SUBCELLULAR LOCATION: Outer-membrane associated or secreted (By
                                                                                                                                                                                                                                                                                                                         modified (By similarity).

MSCELLANDEOUS: Its target cell specificity is restricted to human and some non-human cells of the monomyelocytic lineage. SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                         similarity).
DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                           activity.

DOMAIN: The three transmembrane domains are believed to be involved in pore formation by the cytotoxin (BY SIMILARITY).

PTM: Palmitoylated by lktC. The toxin only becomes active when
                                                                                                                                     Lally E.T., Golub E.E., Kieba I.R., Taichman N.S., Rosenbloom J., Rosenbloom J.C., Gibson C.W., Demuth D.R.; "Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Delineation of unique features and comparison to homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1050;
                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
NCBI_TaxID=714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00330; HEMOLYSIN CALCIUM; 5.
Hemolysis; Toxin; Cytolysis; Repeat; Calcium; Transmembrane;
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                                 Actinobacillus actinomycetemcomitans (Haemophilus
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Pred. No. 1e-78;
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InterPro; IPR001343; Hemlyen_Ca_bind.
InterPro; IPR003995; RtxA.
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                                                                                                                          MEDLINE=89359382; PubMed=2670940;
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PRINTS; PR01488; RTXTOXINA.
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MEDLINE=99214144; PubMed=10196151;
Basar T., Havlicek V., Bezouskova S., Halada P., Hackett M., Sebo P.;
Basar T., Havlicek V., Bezouskova S., Halada P., Hackett M., Sebo P.;
With conserved lyaine 860 in the additional fatty-acylation site of
Bordetella pertussis adenylate cyclase is crucial for toxin function
independently of its acylation status...;
J. Biol. Chem. 274:10777-10793(1999).
-I- FUNCTION: THIS ADENYLATE CYCLASE BELONGS TO A SPECIAL CLASS OF
BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAMMALIAN
CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL
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Munier H., Gilles A.-M., Glaser P., Danchin A., Sarfati R., Barzu O.;
"Isolation and characterization of catalytic and calmodulin-binding
domains of Bordetella pertusais adenylate cyclase.";
Eur. J. Biochem. 196:469-474(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of residues essential for catalysis and binding of calmodulin in Bordetella pertussis adenylate cyclase by site-directed mutagenesis.",
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             Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (ACT) (AC-HLY) [Contains: Calmodulin-sensitive adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin]
                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=18323;
MEDLINE=89091151; PubMed=2905265;
Glaser P., Sakamuco H., Bellalou J., Ullmann A., Danchin A.;
"Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase-haemolysin bifunctional protein of Bordetella pertussis.";
EMBO J. 7:3997-4004(1988).
                                                                                                                                                                                                                                                 MEDLINE-88216178; PubMed=2897067; Glaeer P., Ladant D., Sezer O., Pichot F., Ullmann A., Danchin A.; Glaeer P., Ladant D., Sezer O., Pichot F., Ullmann A., Danchin A.; "The calmodulin-sensities adenylate cyclase of Bordetella pertussis: cloning and expression in Escherichia coli.";
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                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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Adv. Second Messenger Phosphoprotein Res. 27:109-162(1993).
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89251630; PubMed=2542030;
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                                                                                                       Bordetella pertussis.
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                                                                                                                                                                       NCBI_TaxID=520;
                                                                                 CYA OR CYAA.
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            -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
-!- ENZYME REGULATION: ACTIVATED BY HOST-CALMODULIN.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REQUIRED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY (BY SIMILARITY).
-!- PIM: FALMASED IN A PROCESSED FORM.
-!- PIM: PALMITOYLATED IN PROCESSED FORM.
MODIFIED IN POSITION LYS-983.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ADBNYLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyase; CAMP biosyntheeis; ATP-binding; Hemolysis; Toxin; Virulence; Whooping cough; Calcium-binding; Repeat; Lipoprotein; Palmitate. CHAIN CHAIN
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HEMOLYSIN (BY SIMILARITY TO E.COLI HEMOLYSIN HLYA).
                                                                                                                                                                                                                          CYCLASE CLASS-2 FAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
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28 X REPEATS, GLY-RICH.
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B, ALA/GLY-RICH.
C.
D, ASP/GLY-RICH.
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 5.
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HSSP, P40136; 1K90.
InterPro; IPR005165; Anthrax toxA.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001399; RtxA.
Pfam; PP03497; Anthrax toxA; 1.
Pfam; PP00353; hemolysinCabind; 17.
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Page 17

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PRINTS, PRO0313; CABNDNGRPT.
PRINTS, PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM;
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                                                                                                                                                                                                    Alcaligenaceae; Bordetella.
                                                                                                      STANDARD;
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                                           LQDKKDGTV
                                                           1279 MGQGGDDTV
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                                                                  1220 RIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVRNVENVIGTSMKD-VLIGDAQANTL 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    057506; 006179; 01-NOV-1997 (Rel. 35, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) Bifunctional hemolysin-adenylate cyclase precursor (Cyclolysin) (AC-HI) (AC-HIV) (Contains: Calmodulin-sensitive adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl cyclase); Hemolysin].
--KDGSYITSDOIDKI
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Danchin A., Boursaux-Eude C.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-I- PUNCTION: THIS ADENYLATE CYCLASE BELONGS TO A SPECIAL CLASS OF BACTERIAL TOXIN. IT CAUSES WHOOPING COUGH BY ACTING ON MAMMALIAN CELLS BY ELEVATING CAMP-CONCENTRATION AND THUS DISRUPTS NORMAL
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-!- ENZYME REGULATION: ACTIVATED BY HOST CALMODULIN.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: THE GLY-RICH REGION IS PROBABLY INVOLVED IN BINDING CALCIUM, WHICH IS REGULED FOR TARGET CELL-BINDING OR CYTOLYTIC ACTIVITY (BY SIMILARITY).
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-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ADENYLYL.
CYCLASE CLASS-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Betsou F., Sismeiro O., Danchin A., Guiso N.; "Cloning and sequence of the Bordetella bronchiseptica adenylate cyclase-hemolysin-encoding gene: comparison with the Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
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    SINIPRWY - - - ITSNLONYQSNKTD-
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Pfam; PF00353; hemolysInCabind; 17.
Pfam; PF02382; RTX; 1.
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InterPro; IPR001343; Hemlysn_Ca_
InterPro; IPR003995; RtxA.
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1154 WGDDGNDTIHGRGGDDİLRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYSA 1213
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MEDLINE=2017575; PubMed=10710307;
MEDLINE=2017575; PubMed=10710307;
MEDLINE=2017575; PubMed=10710307;
Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Mason T., Ciecko A., Parkey D.S., Blair E., Cittcone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                            LQARH-EQLANSDGLRKMLADLQAGWNASSVIGVQTTEISKSALELAAITGNADNLKSAD
                                                                      593 IFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVK
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YDSRYAAYLANN----LKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGK
                                                                                                            KYSYINKLKF-GRVKNWQVTDGEASSKLDFSKVIQRVAETEGT--DEIGLIVNAKAGNDD
                                                      AYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNG
                                                                                                                                                                                                                                                                              713 EGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDL------LDGGSG-----
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SUBCELLULAR LOCATION: Outer-membrane associated and secreted (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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FPRC OR NMB1415.
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synthesis; ATP-binding; Hemolysis; Toxin; Virulence; Calcium-binding; Repeat; Lipoprotein; Palmitate.
                                                      HEMOLYSIN (BY SIMILARITY TO E.COLI HEMOLYSIN HLYA).
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AA; 177153 MW; C43B330F5886C835A CRC64;
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PALMITATE (BY SIMILARITY)
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                                                                                                ALA/GLY-RICH.
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               Whooping cough;
CHAIN
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                                                                                                                                                                  125 STLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSOSTOTIEAFSSOLA 184
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VIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTET
                                                                                 AKKSVDTVN-QFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVL
                                                                                                                                                                                                         325 A-----DGSAEKAKQVVEDLAQAAKEAYENAKSTAEKAAQAAREFFKGLP
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                           243 IVNNNIKQGNEAFKNEINSL-
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                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
      probably involved in binding target cell-binding or cytolytic
                                                                                                                                                                                                                                                                  EMBL, AE002490; AAF41776.1; -.
PIR; B81086; E81086.
TIGR; NMB1415; -.
INCEPTO; IPRO01343; Hemlyen_Ca_bind.
INCEPTO; IPRO03995; RtxA.
PFAN; PR00313; CABNDWGRPT.
PRINTS; PR00313; CABNDWGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSTITE; PR01488; RTXTOXINA.
PROSTITE; PR01489; TOWLET MEMOLYSIN CALCIUM; 17.
TOXIN; Calcium; Outer membrane; Repeat; Complete proteome.
DOMAIN
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                                                                  SIMILARITY: BELONGS TO THE RIX PROKARYOTIC TOXIN FAMILY
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Pred. No. 2.6e-14;
5; Mismatches 365;
        DOMAIN: The Gly-rich region is calcium, which is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Sc
Best Local Similarity 20.4%; Pr
Matches 227; Conservative 175;
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1041 IYSGNGNDT------LNGGEGNDAL------YGYNGNDALNGG----- 1071
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llarity 21.9%; Pred. No. 3.2e-14;
Conservative 167; Mismatches 355; Indels 302;
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97 1302 23.
1302 23.
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Matches 231; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Outer-membrane associated and secreted.
-!- DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                    Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria.
NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=FAM20 / Serogroup C;
MEDLINE=94018616; PubMed=8412674;
Thompson S.A., Wang L.L., Sparling P.F.;
"Cloning and nucleotide squence of frpC, a second gene foreseria meningitidis encoding a protein similar to RTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; LUGAZON, CALLON BIR, S35027; S35027; S35027; S35027; S35027. InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001395; RtxA.
InterPro; IPR00313; CABNDNGRPT.
PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 17.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 17.
TOXIN; Calcium; Outer membrane; Repeat.
R79 1702 43 X REPEATS, GLY-RICH.
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                                                                                                                                                                                              (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                 | || : : :: || | : ::|:| || DDSGQVTVQSYF-----QNDGSGA--YRIDEIHFDNGKVLDVATVKELVQQSTDG----- 1401
                                                                                                                                                                                                                                                                   LEGGSGSDTYVFGKGFGQDTVYNYDYATGRKDIIRFTDGITAD-MLTFTREGNHLLIKAK 1353
                                                                                                                                                                                                                                            SKFNDIFHSGEGDDLLDGGAGDDRLF-----GGKGNDRLSGDEGDDLLDGGSGDDV 753
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MEDLINE=20175755; PubMed=10710307;
Esten J.A., Katchum K.A., Heidelberg J., Jeffries A.C., Nelson K.E.,
Esten J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark B.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
DHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS
                                                                                                         1115 VYNYDYATGRKDIIRFTDGITADMLTFTREGNHLLIKAKDGSGQVTVQSYFQNDGSGAYR
                                                                                                                                                       TETIQYRDYELRKVG------YGYQSTDNLK---SVEEVIGSQFNDVFKG
                                                                  V------DGTSA----TEAGSY-TVNRKVARGDIYHEVVKRQETKVGKR
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DOMAIN: The Gly-rich region is probably involved in binding
calcium, which is required for target cell-binding or cytolytic
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FRPA OR NMBOSBS.
Beisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Neisseria.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
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| | | | | | | | | ALNIVKVTNDTYDHLAKNIYQNLLFQTRLQPYLNQISFKMENDTFTLDF-SGLVQAFNHV 666
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                                                                                                                                                    PRINTS; PRO1488; KIALCALTION; 9.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 9.
TOXIN; Calcium; Outer membrane; Repeat; Complete proteome.
13 X REPEATS, GLY-RICH.
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                                                InterPro; IPR001343; Hemlysn Ca_bind.
InterPro; IPR003995; RtxA.
                                                                                                 Pfam; PF00353; hemolysinCabind;
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
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Best Local Similarity 22.5%;
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1302 AA;
C81182; C81182.
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us-10-069-799-5.rsp

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                                                               Similarity
                                                                         Matches 239;
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                                                        802
  DVFKGSKFNDIFHSGEGDDLLDGGAGDDRLF------GGKGNDRLSGDEGDDLLDGG
              SGDDVLNGGAGNDVYIFRKGDGNDTLYD---GTG-NDKLAFADANISDIMIERTKEG--I
                                                                                      IVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Outer-membrane associated and secreted. DOMAIN: The Gly-rich region is probably involved in binding calcium, which is required for target cell-binding or cytolytic
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                                                                                                                                                                                                                                                                                                                                                STRAIN=FAM20 / Serogroup C;

BEDLINE=29139051, PubMed=842153;

Thompson 5.A., Wang L.L., West A., Sparling P.F.;

"Neisseria meningitidis produces iron-regulated proteins related to the RTX family of exoproteins.";

J. Bacteriol. 175:811-818(193).

-I- FUNCTION: May participate in the pathogenesis of meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity.
SIMILARITY: BELONGS TO THE RTX PROKARYOTIC TOXIN FAMILY.
                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup C).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                   ------SDRLYAYOSGNTLNGGLGDDYLYG 1098
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lcium; Outer membrane; Repeat.
765 988 13 X REPEATS, GLY-RICH.
                                                                                                                               TVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFG
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                                                                                                                                                                                                                             (Rel. 34, Created)
                                                                                                                                                                                                                                                             Iron-regulated protein frpA
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                                                                                                                                                                                                                                                                                                                                                                                                                    131 LGTALA--GIEL--DSLIKKGDAAPDALAK--ASIDLINEIIGNLSQSTQTIEAFSSQLA 184
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                                                                                                                                                                      Indels 399;
                                                                                                                   Length 1115;
                                                                       122177 MW; 21841065BCCACEFA CRC64;
                                                                                                                                                                   Conservative 171; Mismatches 364;
                                                                                                                     DB 1;
                                                                                                                     Score 408.5; DB 3
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GESSSSTAQVGNISGQGGVELKAGRDLTLQGTDVKSQGDVSLSAGNKVALQAAESTQTRK 1175
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                                                       673 KTGNINVKAAERQQNIDEQKTALTVNGYAKEAGDKQYRAGLRIEHTRDSEKTTRTENSAS 732
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                          DRKLGKASNVLSTL----SSFLGTALAGIELDSLI-----KKGDAAPDALAKASIDLINE 164
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(Rel. 25, Last sequence update)
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                                                                                                                                 -----ISNPDFAKYINAGNNLVQSM 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                 KLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIG 841
                                                                                                                                                                                                 842 KDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSL---NKLVGSM 898
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----GGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYD---GTGND 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 IQAGLNSTKSGLK---NLYLAIPKDYDPQKGGTLNDFIKAADE-----LGIARLAEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM RENTHROCYTE MEMBRANE. SHLA REQUIRES SHLE PUNCTION WITH THE ERYTHROCYTE MEMBRANE. SHLA SEQUIRES SHLE PUNCTION. SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol, 170:3177-3188(1988).
FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Best Local Similarity 20.9%; Pred. No. 0.058;
Matches 220; Conservative 123; Mismatches 406; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                                                                                                                                                                899 ALFG----TANSVSSNALQPITQPTQGILAPS 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1608 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
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Hemolysis; Toxin; Outer membrane; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Serratia
NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M22618; AAA50323.1; -.
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                                                                                                                                                                                                                                                   1061 DDAA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serratia marcescens.
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2009 QKERESEQLAKDATDIYNVIKLKNEFNEKLEEAKNKEEVVSEKVREALKRLSQVEGIRCH 2068
FDSADKSMKSVLPISELGAEKSLDKVKAAKESYEKNLETVQNEMSRINVEEGSLTDIDKK 1732
                                                                                                                                                                                 --ITDIEND------LLKMKKOYEEGL-----LQKIKENADKRKSNFELVG 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1903 TIVDELKTLNDISECSSVLN----NVVSIVKKVKESKHADYRRDAN-SMYE----SMVTL 1953
                                                                                                                                                                                                                                                                  1771 SEINALLDPSTSIFIKLKLKEYDMTGDLKNYGV------KMNEIHGE-----FTK 1814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRK------GDGNDTLYDGTGNDKLAF 785
                                                                                                                                           TGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFG---RVKNWQVTD
                                                                                                                                                                                                                                                                                                           616 DGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKV
                                                           -----ELAGITKLG----ERIKSGK-AYADAFEDGK-----KVEAGSNITLDAK
                                                                                                                                                                                                                            GEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSK
                                                                                                                                                                                                                                                                                                                                                                                            GYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDR
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SUBCELLUTAR LOCATION: Outer membrane.

MAX BE RESPONSIBLE FOR PORE FORMATION.

SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.

STRAIN=Isolate 477-12;

MEDLINE=90170827; PubMed=2407716;

MEDLINE=90170827; PubMed=2407716;

Uphoff T.S., Welch R.A.;

"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB)...;

J. Bacteriol. 172:1206-1216 (1990)...

J. Bacteriol. 172:1206-1216 (1990)...

CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINED. FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LIGKDGSYI----TSDQIDKILQDKKDGTVITSQE----LKKLAD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteus mirabilis.
Bacteria; Proteobacteria; Ga
Enterobacteriaceae; Proteus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 YVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKF----NHANALDEFAK--Q 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRKFGYDG-----DHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPIA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
                                                                                                                                                                                                                                                 -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION, SPECIFICALLY BINDS TO HUMAN RETICULOCYTE CELLS.
-!- SUBUNIT: Homodimer (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDIDDKVK-----KIEGIKREILKMKESALTFWEESEKFKQMCSSHMENAKEGKKKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNINVIKSNIQA-----GLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 ARLAEEPNHT-----ETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQ--AKGFSNI-----GNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1420 SESVRFSQ-----LANGEFTKAEGEEKNASA--RLAEAEKLKEQIV----KDLDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 LANNLKFLSELNKELEAER------VIAITQQRWD--NNIG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $; Score 188.5; DB 1; Length 2869;

f; Pred. No. 0.14;
175; Mismatches 360; Indels 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL ATTACHMENT SITE (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Malaria; Receptor; Signal; Transmembrane.
SIGNAL 1 17 POTEWITAL.
18 2869 RETICULOCYTE BINDING PROTEIN 1.
DOMAIN 18 2807 EXTRACELLULAR.
                                            lasmodium vivax (strain Belem).
ukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
"A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B9DBE442205EBCFF
                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC.
    Reticulocyte binding protein 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                 MEDLINE=92315338; PubMed=1617731;
                                          Belem)
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                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1099 VGTTPESKDYGGGFNA----GTTHHS--KEQTTAKVGTITGS---QGIELNA---GHN 1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GOLLLAADNNVNITGSQVKGNQGAFVKTTQGDVVID-------NALS---E 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKIDERIGIAFNI--TKSS------HKNETNKQTSTGSELISDAQLIVVSGNDVN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 SGI----SAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             689 KEVEDKOYSAGFHITH----TINKNTSTETEQANSTISGANVDLQANKDVTFAGSDLKTTA 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 AVAALITSSIMLAISPLAFMNAADK------FNHANALDEFAKOFRKFGYDGD 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLIN----E 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 IIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNI--GNKLQNLNFSKTNLGLEIITGLL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          746 GNASITGDNV-----AFVSTENKKQTDNTDTTISGGFSYTGGVDKVGSK-ADFQYDKQ 797
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                                                                                                                                                                                                                                                                                                                                                                                                                     509 NLNVQKTNNDKTVTDNHVMWGGIGGGONKNNNNQQQVSHATQLTAD------
                                                                                                                                                                                                                                                                                                                                        325;
                                                                                                                                                                                                                                                                                                   Length 1577;
                                                                                                                                                                                                                                                                                                / Match 3.9%; Score 183.5; DB 1; Length 1 Local Similarity 20.3%; Pred. No. 0.11; ndels nes 211; Conservative 132; Mismatches 371; Indels
                                                                                                                                                                                                                                                           165869 MW; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                               Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                          HEMOLYSIN
                                                                                                                                                         EMBL; M30186; AAA25657.1; -.
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1577 AA;
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                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                       241 LOGAQVNSKDTQL-----ISQSGDIEI----TSAQSTDYKNNWGTD-----IG 1279
                                                                                                                                                                                                                                                                                                                                       1280 FNGK--KTNNTPKEVTEEKPATSIHNIGGKLLVNVEDQQKTSHQNATLETGTLTINSNK- 1336
.145 LTLQGTHLSSEQDIALNATNKVDLQSASSEHTEKGNNLSGGVQAGFGKKMTDDASSVNGL 1204
                                                     GDDRLFGCKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDK 782
                                                                                                                                                                  LAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSN-KTDHKIEQLIG
                                                                                                                                                                                                                                                                               842 KDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQK-----LSASDIASSLNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
-i. SIMILARITY: Contains 13 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00678; WD_REPEATS_1; 3.
PROSITE; PS50082; WD_REPEATS_2; 14.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Hypothetical protein; Repeat; WD_repeat; Complete proteome. REPEAT_1070_1109 WD_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                       GSAQFAIGKODEKSVSREGGTI--NNSGNLTIN---GNSVH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical WD-repeat protein all2124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1683 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | | | | | 1337 -- DLTLSGANVTADSVTGN 1353
                                                                                                                                                                                                                                                                                                                                                                                               VGSMALFG---TANSVSSN 910
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SMART; SM00320; WD40; 14.
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InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00400; WD40; 14.
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Q8YV57;
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                                                               44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1205 FSPDGQT-----IAAGSEDKTVKLWHRQDGKLLKTLNGHQDWVNSLSFSPDGKTLA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1256 SASADKTIKLWRIADGKLVKTLKGHNDSVWDVNFSSDGKAIASASRDNTIKLWNRHGIEL 1315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 LK-TITGHEQTVNNVYFS--PDGKNLASASSDHSIKLWDTTSGQLLMTLTGHSAGVITVR 1204
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                                                                                                          QSYQEQLGG----IKGALERSCQGVYESLPPQLQECAKWI-----FLSLTQLGEGTED 815
                                                                                                                                                                           AAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTI-----SQAKGFSNIG 200
                                                                                                                                                                                             857 ---EAQGKS----FSPTPPNLSTPFVTVEVAHEILIRHWSTLRWWLEENRDRLRKQRQIN 909
                                                                                                                                                                                                                    201 NKLONLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFEL----SNQVIGNV 256
                                                                                                                                                                                                                                         910 HACÓ------LWQQŚGKQADFLL----QGARLAEABDIYIYWTDELGADV 949
                                                                                                                                                                                                                                                               257 TKAISSYVL------AQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD 301
                                                                                                                                                                                                                                                                                                          -KFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAA-A 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVPWVSFSPD--------GKIIASASADKTIRLWDSFSGNLIKSLPAHNDLVYS
                                                                                     31 KDYDPQKGGTLNDFIKAADELGIARLAEE--PNHTETAKKSVDTVNQFLSLTQTGIAISA
                                                                                                                              TKLEKFLOKHSTNKLAKGLDSVENI DRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGD
                                                                                                                                                   816 TRRRIYKSDLIVKKYPAGL------VEQTLNVLTNAKLVVINLEAEI----
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                                                               327;
                                          Length 1683;
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1570 1609 WD 12.
1611 1650 WD 13.
1683 AA; 185459 MW; F7CB36IFF54F7137 CRC64;
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                                          3.9%; Score 180.5; DB 1;
larity 19.6%; Pred. No. 0.17;
Conservative 125; Mismatches 354;
                                           DB 1;
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                                                     al Similarity
197; Conserv
           REPEAT
SEQUENCE
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MEDLINE=PORTON N.A., AND SEQUENCE OF 4-18:

MEDLINE=PORTON SEPT PubMed=2687250;

MADLINE=PORTON SEPT PubMed=2687250;

MAJÍFEALMAN C.A., Wijíjes A.H.M., Spaink H.P., Ruiz-Sainz J.E.,

MAJÍFEALMAN C.A., Okker R.J.H.M., Spaink H.P., Ruiz-Sainz J.E.,

MAJÍFEALMAN C.A., Okker R.J.H.M., Spaink H.P., Ruiz-Sainz J.E.,

MAJÍFEALMAN C.A., Okker R.J.H.M., Spaink H.P., Ruiz-Sainz J.E.,

Indól, a new nod gene of the Rhizobium leguminosarum biovar viciae

Sym plasmid pkiljí, encodes a secreted protein.";

J. Bacteriol. 171:6764-6770(1989).

-I. FUNCTION: THE NODO PROTEIN MAY PLAY A ROLE IN NODULE DEVELOPMENT

SUBCELULAR LOCATION: SECRETED. BY A MECHANISM THAT DOES NOT

SUNCOLES AN VERMINAL SIGNAL PEPTIDE.

-INDÚCTION: BY NARINGENIN (FLANONOID).

-I. SIMILARITY: TO HEMOLYSIN AND RELATED PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGDDRLFGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=9015, PubMed=2303029; BECOROMON A.W.B., Downie J.A.; Economon A., Hamilton W.D.O., Johnston A.W.B., Downie J.A.; The Rhizobium nodulation gene nodO encodes a Ca2(+)-binding protein that is exported without N-terminal cleavage and is homologous to hamolysin and related proteins."; EMBO J. 9:349-354(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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EXPORT SIGNAL (ASPARTIC ACID BOX)
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PRINTS; PR00313; CABNUNGRPT.
PR05SITE; PS00330; HEMOLYSIN CALCIUM; 1.
Plasmid; Nodulation; Calcium-binding; Repeat.
73 8 X APPROXIMATE TANDEM REPEATS.
DOMAIN 92 127 4 X APPROXIMATE TANDEM REPEATS.
---FSPDGRYIASASEDKTVKIWQIDGHLLTT 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobia
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium
NCBI_TaxID=387;
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284 AA; 30002 MW; 9CA41DGFCBDF8E15 CRC64;
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                                                                                                                                                                                                                                                                              01-APR 1990 (Rel. 14, Created)
01-ARR-1990 (Rel. 14, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
NODO OR NOLR.
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                                                                                                                                                                                                                 284
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                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                 STANDARD;
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PIR; S08385; S08385.
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                                                                                                     LTGGDDGDAFVF---RFHDPWVGTTHCYTSVMDFDTKQDRFVLDAADFGGDRNL---FD 172
                                                                                                                                    -- KTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS 867
                                                                                                                                                             ANFINHSKGFPGEFVDTFYNGAAEGAHGEHVVVITDRGFASAAAAATAIDHEARGDIIVF 232
                             --- DGGSGDDVLNGGAGNDVYIFRKGDGNDT 773
                                                                                774 LYDGTGNDKLAFADANISDIMIERT------KEGIIVKRNDHSGSINIPRWYIT 821
NIKGSDNGSFIKGSPENDIIDGGKKNDWIDAGNGDDRIKAGDGQDSITAGPGHDIVWAGK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SETALNE-ATCC 19089 / CB15;

SETALNE-ATCC 19089 / CB15;

MEDLINE-21173699 - DubMed=11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Botocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

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"Complete genome sequence of Caulobacter crescentus.";
                                                      GSDVIHADGGDDLLYSDASYPLYVTDPHRVIPHSGEGDDVLYAGPGSDILV--AGDGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bingle W.H., Awram P.A., Nomellini J.F., Smit J.K.;
"The secretion signal of C. crescentus S-layer protein is located in the C-terminal 82 amino acids of the molecule.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene encoding the Caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
STRAIN=ATCC 19089 / CB15;
MEDLINE=93007489; PubMed=1393820;
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
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                                                                                                                                                                                                                                                                                             D35828; O46015; O9RF12;
01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-F88-2003 (Rel. 41, Last annotation update)
5-layer protein (Paracrystalline surface layer protein)
RSAA OR CC1007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gilchrist A., Fisher J.A., Smit J.K.; "Nucleotide sequence analysis of the gene encoding crescentus paracrystalline surface layer protein." (an. J. Microbiol. 38:193-202(1992).
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                                                                                                                                                                                                          233 HDQKTLGQDGETHGATLAYVDSA 255
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                                                                                                                                                                                                                                                                                    STANDARD;
                            GNDRLSGDEGDDLL
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Caulobacter crescentus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 AMINDLSDGALSTDNAAGVNLFTAYPSSGVS------GSTLSLTTGTDTL---- 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIAT SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205;
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19.2%; Pred. No. 0.11;
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EMBL; AF193063; AAF19365.1; -.
EMBL; AE005779; AAK22991.1; ALT_INIT.
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Pfam; PF00353; hemolysinCabind; 3.
PRINTS; PR00313; CABNDNGRPT.
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TIGR; CC1007
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                                      LVAADATTINISGDARVTITSHTAAALTGITVTNSVGATLGAELATGLVFTGGAGADSIL 640
                                                                                                   684
                                                                                                                              GKYSYINKLKFGRVKNWQVTDGEAS-----SKLDFSKVIQRVAETEGTDEIGLIVNA 586
                                                                                                                                                                                                                                                 694
                                                                                                                                                                                                                                                                                                           753
            YL---ANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFE 482
                                                                      -----NGKKTQALHFTSPLLTAGTESRERLTN
                                                                                                 LGATTKA---IVMGAGDDTVTVSSATLGAGGSVNGGD------GTDVLVANVN
                                                                                                                                                           GS-SFSADPAFGGFETLRVAGAAAQGSHNANGFTALQLGATAGATTFTNVAVNVGLTVLA
                                                                                                                                                                                        KAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDI
                                                                                                                                                                                                                  744 AP-----TGTTTVTLANATGTSDVF------NLTLSSSAALAAGT-----VALAGV
                                                                                                                                                                                                                                                  647 YHEVVKRQETKVGKRTETIQYRDYELRKV-----GYGYQSTDNL-----KSVEEVIGS
                                                                                                                                                                                                                                                                              ETVNIAATDTNTTAHVDTLTLQATSAKSIVVTGNAGLNLTNTGNTAVTSFDASAVTGTGS
                                                                                                                                                                                                                                                                                                         QFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFG-GKGNDRLSGDEGDDLLDGGSGDDV
                                                                                                                                                                                                                                                                                                                                     AVTFVSANTTVGEVV-----TIRGGAGADSLTGSATANDTIIGGAGADTLVYTGGTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 145:115-120(1994).
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuen B., Sleytr U.B., Lubitz W.; "Sequence analysis of the sbsA gene encoding the 130-kDa surface-layer protein of Bacillus stearothermophilus strain PV72.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9F1383AD810C0B0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                     754 LNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISD 792
                                                                                                                                                                                                                                                                                                                                                                                               Fregreadir-----binalgrstarvtitbaavgb 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-layer protein precursor (Surface layer protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
S-LAYER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1228 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                       DGKKVEAGSNITLDAKTGIIDISNS-
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PIR; 140468; 140468.
Signal; Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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BB

Score 175.5; Di Pred. No. 0.21;

3.8%;

Query Match Best Local Similarity

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830
53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDG 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877
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                                                                                                                                                                                                                                                                                                                                                                : :: :| | :| ::| | :: |: ::| | ::| | IPKVT-----DAFKTELTEVAKKALDADE-AALTPKVESVSAINTQNKAVELTAVPVNG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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                                                                                           ----TYIDAY 128
                                                                                                                                           ----IDRKLG 118
                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                     224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 TPIALLV--AGVTG------LISGILEASKQAMFESVAN------RLQGKIL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 E-----WEKONGGON----YFDKGYDSRYA----AYLANNLKFL-----SE 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561
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                                                                                                                                                                                                                                                                                 177 KTTRDLLRSTFKAKAQELRDSLIYDITVAMKAREVQDAVKAGNLDK---AKAAVDQINQY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALITSSIMLAISPLAFMNAAD-KFNHANALDEFAKOFRK----FGYDGDHLLAEYORGV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            333 ITVDAST-----PFENNTEYKVVVKGIKDKNGKEFKEDAFTFKLRNDAVVTQV---F 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GINVTNNTSVNLAAGTFDTDDTLTVVFDKLLAPETVNSSNVTITDVETGKRIPVIASTSG 441
                                            LNSTKSGLKNLYLA-IPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STGSLTTNVWGKLAGGVNEAGTYYPGLQFTTTFATKLDESTLADNFVLVEKESGTVVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAKT------LTAGIESNSNG----KKTQALHFTSPL-----LTAGTESRERLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |: : : | : : | : | : | : | COVAVVKA------GANLSALTASDIIPASVEAVTGQDGTYKVKVAAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SEELKTSSGS--LVGGKVT-----VEKLTNNGWVD----AGTGTTVSVAPKTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            771 ND-----TLYDGTGNDKLAFADANISDIMIERTKEGI-----IVKRNDHSGSINIPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAP
                                                                                                                                                                                                                             ------KASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVI----QRVAETEGTDEIGLIVNAKAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----QLERNQGYKLVVFGK------GATAPVKDAANAN-TLATNYIYTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746 TEGÓDVTAPTVŤKVFK------GÖSLKDADAV--TTLTNVDAGQKFTIQF-
                                                                                                                                                                                                                                                                                                                                     IGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLNFSKT-NLGLEIITGLLSG
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                                                                                                                                           74 NQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVEN------
Indels
                                                                          VYKAGGAKKDAYLADLQKEYETY-----VFKANPKSGEARVA
Conservative 154; Mismatches 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTIEASLTTISTALGA------
  210;
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717 LLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYD 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              837 EQLIGKDGSYITSD-QIDKILQDKKDGTVITSQELK-----KLADENKSQKLSASDIA 888
 -TKVELFHKHET-TISNIFKESEIL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-BECOULS.

MEDLINE-BECOLISES, PubMed=7592325;

Massif C., Cheek D., Belas R.;

Massif C., Cheek D., Belas R.;

Massif C., Cheek D., Belas R.;

Massif C., Cheek D., Belas R.;

Massif C., Cheek D., Belas R.;

Massif C., Cheek D., Belas R.;

Maccardiar analysis of a metalloprotease from Proteus mirabilis.";

I Bacteriol. 177:5790-5798 (1995).

I FUNCTION: ONE OF THE VIRULENCE FACTORS PRODUCED DURING SWARMER CELL DIFFERENTIATION OF THE BACTERIA, WHICH SEEMS TO BE ASSOCIATED WITH PATHOGENESIS THE PROTEASE ACTIVITY IS LIMITED TO IG A1,

IG A2, AS WELL AS IG G DEGRADATION.

I COPACTOR: Binds 1 zinc ion per subunit (By similarity).

I COPACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBCELLULAR LOCATION: Ca(2+) increases protease activity.

I SUBCELLULAR SECRETION OF THIS METALLOPPORTANT IN THE EXTRACELLULAR SECRETION OF THIS METALLOPPORTANT IN THE
                                                                                                                                                                                                                                                                                                                                              597 NLRNASENTSDYNSAKTLRLEAQKEKVNLLNKEEEANKYLRDVKKVESFRFIFNMKESLD
                                                         ELN--KELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNI
                                                                                                                                                                              TLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKL-KFGRVKNWQ
                                                                                                                                                                                                                                                   553 VTDGEASSKLD--FSKVIQRVAETEGTDEIGLIVNAK--AGNDDIFVGQGKMNIDGGDGH
                                                                                                                                                                                                                                                                                    495 VTEKNRINGIDSTITNIEGALKESKGNYEIGPLEKLEEIGKNRKLKVDITKKSINSTVGN
                                                                                                                                                                                                                                                                                                                        DRVFYSKDGGFGNITVDGTSATEAGSYTVNRKV----ARGDIYHEVVKRQETKVGKRTE
                                                                                                                                                                                                                                                                                                                                                                                                664 TIQ-----YRDYELRKV--GYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657 KINEMIKKEQL--------TUNEGHGNVKQLVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
                                   --OAMFESVANRLOGKILEWEKONGGONYFDKGYDSRYAAYLANNLKFLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Extracellular metalloprotease precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to peptidase family M10B
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312 INENIRNSEQYLKDIEDAEKQAS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteus mirabilis.
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                                     388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 GLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHL--LAE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKIELYKKEIDEIKOKTNEYKQGDTSNFYYTEQYNSATQ----SKAKIEQFINIATTKK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKAS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 IDLINEIIGNLSQSTQTIEAFSSQLAK-LGSTISQAKGF-SNIGNKLQNLNFSKTNLGLE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 IITGLLSGISA-----GFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 DKCTTE----ISNS-----KRGKDKI-----BFLEKFKPNEESNSNKVNINE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 YQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALLVAGVŢGLISGILEASK-- 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS HUMAN RETICULOCYTE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.7%; Score 173; DB 1; Length 1251; Best Local Similarity 19.3%; Pred. No. 0.28; Matches 186; Conservative 142; Mismatches 341; Indels 294;
                                                                                                                                                                                                                                                                                        Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                             Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1251 1251
1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AIPKDYDPQKGGTLNDFIKAADELGIARLAEEP----
                                                                                                                                                                              (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                               1251 AA
                                                                                                                                                                                                                                  Reticulocyte binding protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92315338; PubMed=1617731;
                                                                                                                                                                                                                                                                       Belem)
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                                                                                                                                                                                                                                                                       Plasmodium vivax (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                   69:1213-1226(1992).
                                                                                                                                               STANDARD;
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                  SV 927
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TV 973
                                                                                                                                                                                                                   01-OCT-1996
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Cell 69:121
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NON TER
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR001043; Hemlysn Ca bind.
InterPro; IRR006025; NZn MTpeptdse.
InterPro; IRR006025; NZn MTpeptdse.
InterPro; IRR006025; Zn MTpeptdse.
Pfam; PF00153; hemolysinCabind; 3.
PRINTS; PR00313; CABNDNGRPT.
SMART; SM00235; ZnMc; 1.
PROSITE; PS00142; ZINC; PROTEASE; 1.
PROSITE; PS00130; HEMOLYSIN CALCIUM; FALSE NEG.
Hydrolase; Metalloprocease; Znnc; Zymogen; Repeat; Virulence; Calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 AHFQGAYAGAPLLHDISAMQYLYGANTTTRTGDDVYGFNSNTGIDYYTATDSNDKLIFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 LDAKTGIIDISNSNGKKTQALHFTSPLL-----TAGTE-SRERLT-NGKY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 ----SYINKL-KFGRVKNWQVTD---GEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N--DDIFVGQGKMNIDGGDGHDRVF----YSKD----GGFGNITVDGTSATEAGSY
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
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21.0%; Pred. No. 0.12;
cive 75; Mismatches 153; Indels 140;
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54000 MW; 1E6EDEE3F6243A97 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                EMBL; U25950; AAA86729.1; ALT_INIT.
HSSP; P23694; 1SAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 21.0
nes 98; Conservative
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187
190
196
226
393
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METĀL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 -AADELGIAR---LAEEPNHTETA---KKSVDTVNQFLSLTQTGIAI---SATKL---E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSNINVIKS-NIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLN-----DFIK----
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                                                                                                                                                                                                                                                                                                                                                                                                          Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.; "A protective protein antigen of Rickettsia rickettsii has tandemly
                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1900 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAYER WITH HEXACONAL. SYMMETRY.
-!- PTM: GLYCOSYLATED (PROBABLE).
-!- PTM: GLYCOSYLATED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2249;
                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03797; Autotransporter; 1.
TIGRFAMB; TIGR0144; autotrans bari; 3.
Antigen; Repeat; Signal; Cell Wall; S.layer; Glycoprotein. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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OUTER MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 190; Conservative 117; Mismatches 338;
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     2249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 169.5;
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C (TYPE II).
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D (TYPE II)
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                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90354033; PubMed=2117568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M31227; AAA26380.1; -.
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     STANDARD;
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1165
1180
                                                                                                                                                                                                              Rickettsia rickettsii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
OMPA RICRI
P15921;
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---SNVLSTLSSFLGTALAG 137
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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SEQUENCE FROM N.A. STRAIN=MOPn / Nigg;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.; Ghlamydia trachomatis MoPn and Chlamydia
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-!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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llarity 19.1%; Pred. No. 0.58;
Conservative 143; Mismatches 386; Indels 412;
                                                                                                                                                                                                                                pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- SUBCELLULAR LOCATION: CELL WALL SURFACE (ELEMENTARY BODIES)
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Outer membrane; Signal; Multigene family; Complete proteome.
CHAIL 1 20 PROBABLE OUTER MEMBRANE PROTEIN
21 1520 PROBABLE OUTER MEMBRANE DROTEIN
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InterPro; IPR003368; Chlamydia_PMP.
Pfam, PF0379; Autotransporter; 1.
Pfam; PF02415; DUE145; 1.
TIGRFAMS; TIGR01376; POMP_repeat; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AE002286; AAF39070.1; -. PIR; A81731; A81731.
TIGR; TC0197; -.
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les 222; Conserv
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GSESKVPQWI------HVQQGGLELL---HGAILCSYGVK---QDPRAKIVLSAGS 1024
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SLLENIEQSFITATNQTFFLEEEKLPSEAFISAEELSKRRECAGGAIFAKRVYITDNKEP 800
                  TTSDLGQT----DYQGGGALFA-ENISLSENAGAITFKDNIVKTFASNGKMLGG----GAI
                                                                                ERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISN-----SNGKKTQALHFTSPL
                                                                                                                           ----EIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAG
                                                                                                                                                         ALFGKEVAIVQNATVVFEQNRLQCGEQETHGGGG---AVY----GMESASIIGNSFVRFG
                                                                                                                                                                                       -SYTVNRKVARGDIYHEVVKRQE-TKV--GKRTET-----IQYRDYELRKVGYGY----
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                                                             LTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0uter membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Uchiyama T., "Sequencing of the gene encoding the protein rOmp B of Rickettsia japonica.",
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
-STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE PACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swigg Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKASIDLINEIIGNLSQSTQTIEAFSSQLAKLGSTIS-QAKGFSNI----GNKLQNLNFS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 355; Indels 290; Gaps
THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                             SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY LAYER WITH HEXAGONAL SYMMETRY. SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                 120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                   3.6%; Score 167; DB 1; Length 1656; Similarity 19.7%; Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                    168097 MW; 3132A69C9DD5999F CRC64;
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InterPro; IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; I.
IIGRFAMS; IIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 133;
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CHAIN 1339 1656
CHAIN 1339 1656
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1656 AA;
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                                                                                                                           GDEGDD------LLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADAN 789
                                                                                                                                                                                                                       790 ISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLONYOSNKTDHKIEQL------ 839
                                                                                                                                                                                                                                                 800 TADFIASADGTGIVEFVN--TGPIN-----VTLNKQAVPVN----ALKQITVSGPGNVVV 848
                 VDDASSLTNAQTLTISGTIGIIGANNTTLGQFNIGSSKTTLNG--GNVAINELVIGNNGS 654
                                                    SATEAGSYTVNR---KVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYGTDN 684
                                                                                                           LKSVEEVIGSQFNDVFKGSKFND1FHSGEGDDL-----LDGGAGDDRLFGGKGNDRLS 737
                                                                                                                                                                                          752 GTVGGQQGNKFNTVALDNGTTVKFL----GNATF----NGNTTI---AANSTLQISGNY 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=8925387; PubMed=2722818;

Delepelaire P., Wandersman C.;

Delepelaire P., Wandersman C.;

Protease secretion by Erwinia chrysanthemi. Proteases B and C are synthesized and secreted as zymogens without a signal peptide.";

J. Biol. Chem. 264:9083-9089(1989).

-!- COPACTOR: Binds 1 zinc ion per subunit. Magnesium and calcium increase protease activity significantly above the control value.

-!- SUBCELLUIAR LOCATION: Secreted.

-!- SUBCELLUIAR MEDALIOPROTEASE.

-!- SERRETTON OF THIS METALLOROPTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delepelaire P., Wandersman C.;
Protein secretion in Gram-negative bacteria. The extracellular
metalloprotease B from Erwinia chrysanthemi contains a C-terminal
secretion signal analogous to that of Escherichia coli alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
582 LIVNAKAGNDDI FVGQGKMNI DGGD----GHDRVFYSK---DGGFGNI TV---
                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
1-NOV-1991 (Rel. 20, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Secreted protease C precursor (EC 3.4.24..) (ProC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-59 FROM N.A., AND PARTIAL SEQUENCE.
                                                                               VOFAHNTYLI TRITINAAGOGKI I FNPVVNNNTTLAAGT
                                                                                                                                                                                                                                                                                                                                                                             479 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 265:17118-17125(1990)
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=B374;
MEDLINE=91009140; Pubmed=2211614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M59229; AAA24860.1; -. BMBL; J04736; AAA24862.1; -.
                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                             --IGKDGSY 846
                                                                                                                                                                                                                                                                                                       849 NEIGNAGNY 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                          PRTC_ERWCH
P16317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hemolvain.
                                                     628
                                                                                                                                                                 738
                                                                                                                                                                                                                                                                             840
                                                                                                                                                                                                                                                                                                                                                              PRTC_ERWCH
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645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 PGNYQ---GAGSSWYNYN----QSNIRNPGSEEYGROTFTHEIGHALGLAHPGEYNAGEGD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 PSYNDAVYAEDSYQFSIMSYWGENETGADYNGHYGGAPMIDDIAAIQRLYGANMTTRTGD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 IYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLK----SVEEVIGSQFNDVFK 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSKFNDIFHSGEG--DDL--LDG-----GAGDDRLFGGKGNDRLSGDEGDDLLDGGSGD 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVLYGGAGADT--LYGGAGRDTFVYGSGQDSTVAAYDWIADFQKGIDKIDLSAFRNEGQL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLAN 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 -NLKFLSELNKELEAERVIAITOORWDNNIGELAGITKL-GERIKSGKAYADAFEDGKKV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 EAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGR 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 SVY------GFNSNT--DRDF-----YTATDSSKALIFSVWDAGGTDTFD-FS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           752 DVLNGGAGNDVY1FRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRND---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 VKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIG-LIVNAKAGNDDIFVGQGKMNIDGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GHDRVFYSKD--------GGFGNITVDGTSATEAGSYTVNRKVARGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTVNGKTSY--SIDQAAAQITRENVS-----W----NGTNVFGKS-----AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::| :: | :: | SFVQDQFTGKGQEVMLQWDAANSITNLWLHEAGHSSVDFLVRIVGQAAQSDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HSGSINIPRWYITSNLQNYQSNKTDH-KIEQLIGKDGSYITSDQI
                                                                                                                                                                                                                                                                                                                                       SECRETED PROTEASE C.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
LOC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
5 X REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 479;
                                                                                                                                                                                                                                                                           Hydrolase; Metalloprotease; Zinc; Zymogen; Calcium; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   990ED8376725DF61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%; Score 165; DB
                                                                                                                                                                                     Pfam; PF00353; hemolysinCabind; 3.
SMART; SM00235; ZnMC; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 1.
                                                                                                                         InterPro; IPR001343; Hemlysn Ca bind.
InterPro; IPR006026; NZn MTpeptdse.
InterPro; IPR006025; Zn MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51600 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                          LGO8; 17-OCT-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                         MEROPS; M10.054;
                                                                                                                                                                                                                                                                                                   D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Sim
Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370
                                                                                                                                                                                                                                                                                                                                                                                  ACT SITE
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 607
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                                                                                                                                                                                                                                                                                                                        PROPEP
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PIR;
PDB;
PDB;
PDB;
PDB;
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                                                                                                                                                                                                                                                                                                                                                         392 SLSSAPDTITDFORGEDRIDLSAFNKNHDLRFVDNFSGKGNEVVLNW----DSOSHOTNM 447
               RGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYQSTD 683
                                                                                                                              214 YAEDTRQFSIMSYWNEGYTGGDFHGYHAAAPHDIAAIQKLYGANMSTRTGDTVYGFHSNS 273
                                                                                                                                                                                                       274 GRDFYTATDSKTPLIFSVWDAGGNDTFDFSGYSANQRISLISGTFSDVGGLKAMVSIAAG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 173:989-996(1991).

-I. Bacteriol. 173:989-996(1991).

-I. FUNCTION: PRODUCTION OF EXPRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SUPRACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-I. CAPLYTIC ACTIVITY: Sucrose + {(1,6) -alpha-D-glucosyl} (N+1).

-I. SUBCELLULAR LOCATION: Secreted.

-I. DISBASE: DENTAL CARIES.

-I. MISCELLANBOUS: GTP-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES MATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
                                                                                                                                                                                                                                                                    334 AVIENAIGGSGHDVIVGNLSDNRIDGGAGNDVLYGDGGAD--ILTGGAGKDIFVYAWEKD
                                                   162 AWFNYNQADNQRPDINEFGRNTLTHE-----IGHTLGLYHPGDYDASDGNPGYKDVT
                                                                                                                                                                                                                                               725 ---DRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGND
                                                                                                                                                                                                                                                                                                                        782 KLAFADANISDIMIERTKEGIIVKRNDH-----SGSIN--IPRWYITSNLQNYQSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glucosyltransferase-I precursor (EC 2.4.1.5) (GTF-I) (Dextransucrase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Peptide sequences for sucrose splitting and glucan binding within Streptococcus sobrinus glucosyltransferase (water-insoluble glucan synthetase).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=6715 / Serotype G;
MEDLINE=91123227; PubMed=1704006;
Abo H.., Matsumura T., Kodama T., Ohta H., Fukui K., Kato K.,
Kagawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus downei (Streptococcus sobrinus).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 16 cell wall binding repeats.
                                                                                        684 NLKSVEEV-IGSQFNDVFKGSKF-----NDI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1592 AA
                                                                                                                                                                    714 GDD-------LLDGGAGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Sucrose 6-glucosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                                                                 832 TDH 834
                                                                                                                                                                                                                                                                                                                                                                                                                                      448 WLH 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTF2_STRDO
P27470;
                 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484 GKKVEAGSNITLDAKTGIIDI-----SNSNGKKTQALHFTSPLLTAGTESRERLTNGK 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTKLALQSWADVANVIFSEAKDGERATIQFGNYTLIPDGNIDNNSQAFGFYPGNWKWAGS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                  Ghigo J.-M., Wandersman C.;

"A fourth metalloprocease gene in Erwinia chrysanthemi.";

Res. Microbiol. 143:857-867(1992).

-!- COFACTOR: Binds 1 zinc ion (By similarity).

-!- SUBCELDULAR LOCATTON: Secreted.

-!- DOMAIN: THE GLY-RICH REPEATS MAY BE IMPORTANT IN THE EXTRACELLULAR

-SECRETION OF THIS METALLOPROCEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 YSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OGKMNIDGGDGHDRVFYS--KDG-----GFGN--ITVDGTSATEA---GSYTVNRKVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECRETED PROTEASE G.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
4 X 6 AA REPEATS, GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 164.5; DB 1; Length 475; 20.5%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001343; Hemlyan Ca bind.
InterPro; IPR006026; NZn MTpeptdae.
InterPro; IPR006026; NZn MTpeptdae.
InterPro; IPR006025; Zn MTpeptdae.
PERNYS; PR00331; CABNDNGRPT.
SMART; SM00235; ZnMc; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS00143; AMOINSIN CALCIUM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2AD73D9A617F80B7 CRC64;
                                 01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Secreted protease G precursor (EC 3.4.24.-) (ProG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to peptidase family M10B
                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS
475 AA
PRT;
                                                                                                                                                                                                                                                                  MEDLINE=93234866; PubMed=1299839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51577 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X71365; CAA50501.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99; Conservative
STANDARD;
                                                                                                                                  Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S48132; S48132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P23694; 1SAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; M10.055;
                                                                                                                                                                                         NCBI_TaxID=556;
ERWCH
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METĀL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
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918
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z11505; CAA77581.1; -. PIR; G88545; G88545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MormPep; F59B2.12; CE01024.
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                       F59B2.12.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 171; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wohldman P.;
                                                                                                                                                                                                                                                                CAEEL
                                                                                                                                                        1504
                                                                                                                                                                               869
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Matches
                                                                                                                                                                                                                                          RESULT 36
YMJB CAEEL
                                                                                                                                                                                                                                                                YMJB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 NGYQQPGNDWRYFKDGNWA--VGLTTVDGNVQ----YFD--KDGVQAKDXIIVTRDGKVR 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1234 G------AQTVGKQKLYFEANGQQVKGDFVTSDEGKLYFYDVDSGDMWTDTFIEDK 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1284 AGNWFYLGKDGAAVTGAQTIRGQKLYFKANGQQVKGDIVKGTDGKIRYYDAKSGEQVFNK 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .043 NVASDTLFLPSSLLGKVVESGIRYDGKGYIYNSSÄTGDQVK-----ASFITEÄGNL 1093
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                                                                                                                                                                                                                                                                 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 GTIEASLTTISTALG-AVSAGVSAAVG----SAVGTPIALLVAGVTGLISGILEASKQ 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1094 YYFGK-----DGYMVTGAQTINGANYFFLENGTALRNTIYTDAQGNSHYYANDGKRYENE
                                                                                                                                                                                                                                                                                      NSTKSGL-----KNLYLAIPKD-----YDPQKGGTLNDFIK--AADELGIARLAEEPNHT
                                                                                                                                                                                                                                                                                                      DASKAGLVKRTDENGYLYFLNDDLKGVANPQVSGFLQVWVPVGAADDQDI-RVAA----S
                                                                                                                                                                                                                                                                                                                                                            DTASTDGKSLHQDAAM------DSRVMFEGFSNFQSFATKEEEYTNV
                                                                                                                                                                                                                                                                                                                                                                                    L--STLSSFLGTALAGIEL-----DSLIKKGDAAPD----ALAKASIDLINE
                                                                                                                                                                                                                                                                                                                                                                                                         848 VIANNVDKFVSWGITDFEMAPOYVSSTDGOFODSVIONGYAFTDRYDLGMSKAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                  IIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKL--QNLNFSKTNLGLEIITGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 AMFESVANRLQGKILEWEKQNGGQNYF--DKGYDSRYAAY--LANNLKFLSELNKELEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 RVIAITQQRW----DNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 IIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 DGGFGNITVDGTSATEAGS-----YTVNRKVARGDIYHEV---VKRQETKVGKR--TE
                                                                                                                                                                                                                                                                  Gaps
                                                           Transferase; GlycosyItransferase; Signal; Repeat; Dental caries
                                                                                                                                                                                                                                       1.5%; Score 163.5; DB 1; Length 1592; al Similarity 21.0%; Pred. No. 1.2; 209; Conservative 130; Mismatches 384; Indels 271;
                                                                                GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE)
GLUCAN-BINDING (APPROXIMATE)
                                                                                                                                                                                                      (INCOMPLETE).
BCOA66D079351ECF CRC64;
                                                                                                                    TANDEM REPEATS
                                                                         POTENTIAL.
 EMBL; D90213; BAA14241.1; -...
InterPro; IPR002479; CW binding.
InterPro; IPR003318; Glyco_hydro_70.
Pfam; PF01473; CW binding_1; 1...
Pfam; PF02324; Glyco_hydro_70; 1.
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Best Local
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DOMAIN
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REPEAT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                              1456 NKSVTVNGKTÝYF----GNDGTAQTAGNPKGQTFKDG--SDIRF-YSMEGQLV----TG 1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S----GWY--SNAQGQWLYVKNGKVLTGLQTVGSQRVYFDENGI-----QAKGKAVRTSD 1552
                                                                                                                                                                                                                                                                                                                                                             SINIPRWYITSNLON---YQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQ 868
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                                                                                                                                                                                 NGG--AGNDVYIFRKGDGNDTLYDGTGNDK-LAFADANISDIMIERTKEGIIVKRNDHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Sims M., Smaldon M., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oŧ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%; Score 163; DB 1; Length 918; larity 18.5%; Pred. No. 0.59; Conservative, 133; Mismatches 358; Indels 26
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----FHSGE---GDDLLDGGAGDDRLFGGKGNDRLSGD--EGDD
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SEQUENCE 918 AA; 96560 MW; E464FD86B14945DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein F59B2.12 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKKLADENKSQKLSASDIASSLNKLVGSMALFG 902
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Craniata, Vertebrata, Euteleostomi; Catarrhini; Hominidae, Homo.

Chordata; Primates;

Eutheria;

NCBI_TaxID=9606; SEQUENCE FROM of the adhesive

an M.C., Tizard R., Vandevanter D.R., Carter W.G., loning of the Lami3 gene encoding the alpha 3 chain gand epiligrin. Expression in wound repair."; Biol. Chem. 269:22779-22787(1994).

MEDLINE=94357926; PubMed=8077230;

Ryan M.C., "Cloning ligand ep B

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SEQUENCE OF 1-1331 FROM N.A.

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                                    -----AVSAGVSAAGVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVAN 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDN 456
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                                                                                                                                                                   261 QGNKKSQNYSKKAASASGSNADFESNLESLKNADGTSMSNSTGNFNNTSYDKATAEEVWS
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-- IIGNLSQSTQTIEAFSSQLAKLGSTIS
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KERATINCCYTES.
SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulide bonds into a cross-shaped molecule Comprising one long and three short arms with globules at each end. The alpha-3 chain is a subunit of laminin-5 (epiligrin/Kalinin/nicein), and possibly also a component of laminin-6 (K-laminin) and laminin-7 (KS-laminin).
SUBGELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2; Name=A;

Name=B; IsoId=Q16787-2; Sequence=VSP_003037; IsoId=Q16787-1; Sequence=Displayed;

Note=Sequence incomplete;
TISSUE SPECIFICITY: SKIN; RESPIRATORY, URINARY, AND DIGESTIVE
EPITHELIA AND IN OTHER SPECIALIZED TISSUES WITH PROMINENT
SECRETORY OR PROTECTIVE FUNCTIONS. EPITHELIAL BASEMENT MEMBRANE,
AND EPITHELIAL CELL TONGUE THAT MICRATES INTO A WOUND BED. A
DIFFERENTIAL AND FOCAL EXPRESSION OF THE ALPHA-3 CHAIN IS OBSERVED

MEDLINE=96463880; PubMed=8566427;
Midal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
Vidal F., Baudoin C., Miquel C., Galliano M.-F., Christiano A.M.,
Vidal F., Baudoin C., Miquel C., Galliano Gene (LAWA3) and identification
of a homozygous deletion in a patient with Herlitz junctional
general S. 273-280(1955).
C. --- FUNCTION: Binding to cells via a high affinity receptor, laminin
is thought to mediate the attachment, migration, and organization
of cells into tissues during embryonic development by interacting
with other extracellular matrix components.
C. --- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
C. --- FUNCTION: LAMININ-5 IS THOUGHT TO BE INVOLVED IN (1) CELL ADHESION
C. --- FUNCTION: LAMININ-5 IS THOUGHT TO BE ADHESION AND INTEGRIN ALPHAC. FUNCTION: OF PP125-FAX AND PR0, (3) DIFFERENTIATION OF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN THE CNS.
-!- IMDININ-5 IS UP-REGULATED IN WOUND SITES OF HUMAN SKIN.
-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
-!- MITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DOMAIN: DOMAIN G IS GLOBULAR.
-!- DOMAIN: DOMAIN G IS GLOBULAR.
-!- DISABE: DEPECTS IN LAWAS ARE A CAUSE OF JUNCTIONAL EPIDERMOLYSIS
BULLOSA (JEB) GRAVIS, ALSO KNOWN AS HERLITZ TYPE JEB. IT IS A
BLISTERING DISORDER IN SKIN THAT IS CHARACTERIZED BY A SEPARATION
OF BASAL CELLS FROM THE BASEMENT MENBRANE DUB TO A DECREASED
NUMBER OF HEMIDESWOSOMES. LAMININ-S IS MISSING FROM THE BASEMENT
MEMBRANE OF PATIENTS WITH THE GRAVIS FORM OF EPIDERMOLYSIS
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LMA3 HUMAN STANDARD; PRT; 1713 AA.

1016787; 013689; 013680;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
1-SSP-2003 (Rel. 42, Last annotation update)
1-Aminin alpha 3 chain precursor (Epiligrin 170 kDa subunit) (E170)

LMA3 HUMAN

sapiens (Human)

Homo

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                                                                                                                                                     VDTVNQFLSLTQTGIAISATKLE------KFLQKHS-----TNKLAKG 106
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                                                                                                       PKDYDPQKG-----GTLNDF1KAADELG1------ARLAEEPNHTETAKKS
                                                                                                                            PKDSSPAEECDDCDSCVMTLLNDLATMGEQLRLVKSQLQGLSASAGLLEQMRHMETQAK-
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                                                                               Gaps
                                                    Query Match 3.5%; Score 163; DB 1; Length 1713; Best Local Similarity 20.0%; Pred. No. 1.4; Matches 205; Conservative 120; Mismatches 333; Indels 360;
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1184 1184 G -> A (IN REF. 2).
1713 AA; 189304 MW; 45EA9BE1017B60D3 CRC64;
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FRPS -> KVSSYGGYLTYQAKSFALPGDMVLLEKKPDVQL
TGQHMSIIYEETNTPRPDRLHHGRVHVVEGNFRHASSRAPV
SREELMTVLSRLADVRIQGLYFTETQRLTLSEVGLEEASDT
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W -> R (IN REF. 2).
ATG -> GMC (IN REF. 2).
R -> L (IN REF. 2).
R -> L (IN REF. 2).
E -> Q (IN REF. 2).
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Matches 124;
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Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makinoto K., Mizubuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Taqami H., Takeda J., Takeuchi Y., Mamanoto Y., Horiuchi T., Fakeuchi Y., Makauchi Y., Makauchi Y., Bashimoto Y., Horiuchi T., Takeuchi Y., Bashimoto Y., Horiuchi T., Carresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                     MEDIJUE=97426677; PibMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.
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MEDLINE=92190338; PubMed=1665988;
MOSZER I., Glaser P., Danchin A.;
"Multiple IS insertion sequences near the replication terminus in
                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                            YDBA ECOLI STANDARD; PRT; 2003 AA. P33666; P76087; P76088; P76886; P76857; P76859; P7EB-1994 (Rel. 28, Created) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
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EMBL; AE000237; AAC74487.1; ALT SEQ.
EMBL; D90778; BAA15009.1; ALT SEQ.
EMBL; D90779; BAA18880.1; ALT SEQ.
EMBL; D90779; BAA18881.1; ALT SEQ.
EMBL; XC2680.; YOT ANOTATED CDS.
ECGGENE; EG11307; YGBA.
Hypothetical protein; Complete protecome.
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MEDLINE=97251357; Pubmed=9097039;
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Biochimie 73:1361-1374(1991)
                                                                                                                                                                                                                                            Hypothetical protein ydbA.
YDBA OR B1401/B1405.
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STRAIN=K12 / MG1655;
                                                 837 EQLIGK 842
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                                                                                                                                                                                                                     NLWQIDEANNTVALEGVSADGATKWQYNHN-----GELVITG------DNATVNN 228
                                                                                                                                                                                                                                                                                                SMGIQIDGDKAIVNNEGESTITNGGTGTQINGDDATANNNGKTTV-----DGKDSTGTB 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 VNAKAGNDDIFVGQGKMNIDGG------DGHDRVF 612
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                                                                                    3.5%; Score 162.5; DB 1; Length 2003; 20.4%; Pred. No. 1.8; Artive 75; Mismatches 197; Indels 213; Gaps
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STRAIN=VPI 10463;
MEDLINE=99326540; PubMed=2374729;
MEDLINE=99326540; PubMed=23.74729;
MIDLINE=99326540; Wilkins T.D.;
"Nucleotide sequence of Clostridium difficile toxin B gene.";
Nucleic Acids Res. 18:4004-4004(1990).
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
489 I -> V (IN REF. 2).
495 I -> V (IN REF. 2).
; 205949 MW; B83A12C8B53220EE CRC64;
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01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                               | | | | :: | :: | :: | 1.88 BIN---FSGE----VNGSNGFVSLTPSILEGINAIIEVDLLSKSYKLLISGELKILMLNS 1440
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: | : | : | : | : | TKVVDYFKHVSLVETEGVFTLLDDKIMMPQDDLVISEIDFNNNSIVLGKCEIWRREGGSG 1177
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                                                                                                                                                      DNNIGELAGI -----FKLGERIK---SGKAY-----ADA------FEDGKKVEA 489
                                                                                                                                                                                                                                          GSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTE-SRERL-----TNGKYSYINK 542
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence protein pmp21 precursor (Polymorphic membrane protein 21).
18-OCT-2001 (Rel. 40, Last sequence protein pmp21 precursor (Polymorphic membrane protein 21).
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                                                                                                                                                                                                                                                                                        MOl. Gen. Genet. 233:260-268(1992).
-!- DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN ENTEROTOXIN
CALLED A AND CYTOTOXIN B.
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                                                                                                                                                                                                      Schulze J.,
                                                                                                                                                                                                                                            "Comparative sequence analysis of the Clostridium difficile toxins and B.\,^{"}_{\ \ i},
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                                                                                                                                                                                                   Eichel-Streiber C., Laufenberg-Feldmann R., Sartingen S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 18.4%; Pred. No. 2.6;
Matches 223; Conservative 164; Mismatches 375; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2366 AA; 269709 MW; E1024BD8B8A56ADF CRC64;
                                                                                           Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
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18.4%; Pred. No. 2
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Pfam; PF01473; CW_binding_1; 17.
Pfam; PF04488; Gly_transf_sug; 1.
                                                                                                                                                        STRAIN=VPI 10463;
MEDLINE=92293124; PubMed=1603068;
                                                                                                                                    SEQUENCE OF 1271-2366 FROM N.A.
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                                             STRAIN=VPI 10463;
von Eichel-Streiber C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A27636; A27636.
PIR; S10317; S10317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                MEDLINE=20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Bisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20330349; PubMed=10871362; MEDLINE=20330349; PubMed=10871362; Minoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; MCGL020; MCGL020 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).
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TIGRFAMS; TIGRO1376; POMP repeat; 13.
Outer membrane; Signal; Multigene family; Complete proteome.
SIGNAL 31 1609 PROBABLE OUTER MEMBRANE PROTEIN
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1609 AA; 170865 MW; 2604C3E9FC4024CB CRC64;
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21.0%; Pred. No. 1.7
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InterPro; IPR005546; Autotransporter.
InterPro; IPR003368; Chlamydia_PMP.
Pfam; PF03797; Autotransporter; 1.
Pfam; PF03415; DUF145; 1.
                                                                                                                                                                                                                                                                           Nucleic Acids Res. 28:1397-1406(2000)
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EMBL; AE002248; AAF38684.1; --
EMBL; AP002548; BAA99171.1; --
PIR; A86611; A86611.
PIR; H72013; H72013;
PIC; CP0897; --
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                                                         289 VVTHCGDVTLTDCATGLDLEALRLVKDFSRGGAVFTÅRNHEVQNNLAGGILSVVGNKGAI 348
                                                                                                                                                                                                                                     FNHANALDEFAKOFRKFGYDGDHLLAEY ---- ORGVGTIEASLTTISTALGAVSAGV--- 355
                                                                                                                                                                                                                                                                                               FSGNOSLIALGEHIGLTDFVGGGALAAQGTLTLRNNAVVQCVKNTSKTHGGAILAGTVDL 466
                                                                                                                                                                                                                                                                                                                                                     -----SAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKIL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----EWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRW- 454
--INLGLEIITGLLSGISAGFALADKNASTGKKV--AAGFELSNQVIGNVTKAISS--YV 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DUNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RQETKVG----KRTETIQYRD----YELRKVGYGYGYGYGYGYGYGYGYGYGYGYGYGYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    845 ----ENFVFGSENORSGGAIIANSSVNIQDNAGDILFVSNSTGSYGGAIFVGSLVASEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 742 DD----LLDGGSGD------DVLNGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    901 SNPRTLTITGNSGDILFAKNSTQTAASLSEKDSFGGGAIYTQNLKIVKNAGNVSFYGNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --GNDVYIFRKGD-----GNDTLYDGT------GNDK-----LAFADANI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                791 SDIMI---ERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                849 SDQIDKILQDK--KDGTVITSQE----LKKKLADENKSQ-KLSASDIASSLNKLVGSMALF
                                                                                                                                                                                                                                                                                                                                                                                                               467 NETISEVAFKONTAALTGGALSANDKVIIANNFG------EILFEQNEVRNHGGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GKKTQAL--HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEA-SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619 DVVFKGNKGÓCLAQKYVAPQETÁPVESDASSTNKDEKSLNACSHGDHYPPKTVEEEVPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKFNDIFHSGEGDDLLDGGA-----GDDRLF-----GGKGN----DRLSGDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           561 KLDFSKVI------QRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGD-
                                                                                                                  LAQRVAAGLSTTGAVA------ALITSSIMLAISPLAFMNAAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: February 17, 2004, 10:13:48
Job time : 31 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTANS----VSSNALQPITQPT 919
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GenCore version 5.1.6
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                  Copyright
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sw model using protein search, OM protein February 17, 2004, 10:09:49; Search time 27 Seconds (without alignments) 3301.791 Million cell updates/sec Run on:

US-10-069-799-5 4647

1 MSNINVIKSNIQAGLNSTKS.....ssnalQPITQPTQGILAPSV 927 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 80

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			071,137,100	
Result		Query				
No.	Score	Match	Length	B	Ωī	Description
-	2325	50.0	953	-	B30169	leukotoxin A - Pas
7	2236.5	48.1	926	-	B33389	toxin II - Actinob
m	2236	48.1	955	-	A35254	leukotoxin A - Pas
4	2205.5	47.5	926	٦	A43834	toxin II - Actinob
Ŋ	1955.5	42.1	1052	٦	B49219	toxin III - Actino
9	1924	41.4	1049	ч	S51784	toxin III - Actino
7	1847.5	39.8	1024	~	S10056	hemolysin A - Esch
60	1845	39.7	1023	~	LEECA	hemolysin A - Esch
Q	1816	39.1	1055	-	A37205	leukotoxin A - Act
10	1763.5	37.9	1022	Н	I39643	RTX-toxin I - Acti
11	1748	37.6	966	~	T00227	hemolysin A toxin
12	1729	37.2	966	7	141078	hemolysin - Escher
13	805.5	17.3	1705	7	S51672	adenylate cyclase
14	802	17.3	1706	٦	OYBRC	cyclolysin - Borde
15	437	9.4	1829	7	E81086	
16	435	9.4	1829	~	S35027	
17	421	9.1	1302	2	C81182	iron-regulated pro
18	415	8.9	1636	7	B82736	hemolysin-type cal
19	411	8.8	1208	7	C82779	hemolysin-type cal
20	408.5	8.8	1115		A47058	Fe-regulated RTX c
21	391	8.4	2064	~	G82562	bacteriocin XF2407
22	383	8.2	208	~	S34238	leukotoxin A - Pas
23	366	7.9	697	~	F81856	probable RTX-famil
24	344	7.4	4936	~	AH2515	hypothetical prote
25		7.1	1944	~	AH3098	rhizobiocin/RTX to
26	330.5	7.1	1990	7	A96188	probable phosphoes
27	329	7.1	1296	~	C82521	hemolysin-type cal
28	305.5	9.9	993	~	σ	outer membrane sec
29	301.5	6.5	1072	7	G95851	probable hemolysin

30 288 6.2 1417 2 AG2137 31 287.5 6.2 3083 2 AH2493 32 280 6.0 643 2 AG2137 34 276 5.9 650 2 G8752 35 269.5 5.8 1112 2 H9594 36 266.5 5.8 387 2 B9595 39 266.5 5.7 589 2 AD2263 4 266.5 5.7 348 2 AD2263 4 265.5 5.7 348 2 AD2263 4 262.5 5.6 1428 2 AD2263 4 262.5 5.6 1741 2 S74910 4 262.5 5.6 1741 2 S74910 4 262.5 5.6 1741 2 S74910 4 262.5 5.6 1741 2 AP2224	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	calcium-binding pr	probable outer mem	hypothetical prote	hypothetical calci	hypothetical prote	hypothetical prote	probable calcium-b	hypothetical prote	hemolysin - Synech	mannuronan C-5-epi	hypothetical prote	probable outer mem
๛๛๛๛๚๛๛๛๛๛๛๛๛๛ ๘๘๐๐๛ฃฃฃ๛ <i>๛</i> ๛๛๛๛๛	AG2137	AH2493	T03518	AC1852	G87572	H95964	G95405	E95995	AD2263	AD1841	E95933	AC2224	S74910	S77626	AH2137	T03516
	7	~	~	7	~	7	~	7	~	~	7	~	~	7	~	0
•	1417	3083	643	900	650	1112	539	387	589	2348	387	1428	1741	1839	3262	1028
30 288 31 287.5 32 280 34 276 35 269.5 37 267.5 38 266.5 40 266.5 41 262.5 42 262.5 44 262.5 45 262.5	6.2	6.2	6.0	6.0	5.9	5.8	9.8	5.8	5.7	5.7	5.7	5.6	9.6	5.6	2.6	5.6
0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2	288	287.5	280	280	276	269.5	268	267.5	266.5	266	263.5	262.5	262.5	262.5	262.5	261
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1	1
B30169	
leukot	leukotoxin A - Pasteurella haemolytica (serotype 1)
N;Alte	N;Alternate names: lktA protein
C;Spec	C;Species: Pasteurella haemolytica
C; Date	C.Date: 12-Oct-1989 #sequence revision 15-Nov-1996 #text change 18-Jun-1999
C; Acce	C; Accession: B30169; C32051; S29516
R, High	R;Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8	DNA 8, 15-28, 1989
A; Titl	A, Title: DNA sequence of the Pasteurella haemolytica leukotoxin gene cluster.
A, Refe	A. Reference number: A30169; MUID:89210283; PMID:2707120
A, Acce	A; Accession: B30169
A,Stat	A;Status: not compared with conceptual translation
A;Mole	A; Molecule type: DNA
A, Resi	A;Residues: 1-953 <hig></hig>
R,Stra	R;Strathdee, C.A.; Lo, R.Y.C.
J. Bac	J. Bacteriol. 171, 916-928, 1989
A; Titl	A; Title: Cloning, nucleotide sequence, and characterization of genes encoding the secret
A;Refe	A; Reference number: A32051; MUID:89123172; PMID:2914876
0004	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

A;Accession: C32051 A;Status: not compared with conceptual translation

A,Molecule type: DNA A,Residues: 947-953 <STR> R;Lo, R.Y.C.; Strathdee, C.A.; Shewen, P.E. Infect. Immun. 55, 1987-1996, 1987 A;Title: Nuclectide sequence of the leukotoxin genes of Pasteurella haemolytica Al. A;Reference number: S29515; MUID:87306837; PMID:3040588 A; Accession: S29516

A;Molecule type: DNA
A;Residues: 1-741,'D',743-953 <LOR>
A;Cross-references: EMBL:M20730; NID:g150492; PIDN:AAA25529.1; PID:g150494
C;Comment: This organism causes bovine pneumonic pasteurellosis (shipping fever).
A;Genetics:
A;Gene: lktA
C;Function:

A; Description: lyses leukocytes C; Superfamily: hemolysin A; hemolysin A homology C; Superfamily: hemolysin A; hemolysin B homology C; Stywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat; F; 238-784/Domain: hemolysin A homology <HLXA-F; 716-807/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F; 554/Binding site: palmitate (Lys) (covalent) #status predicted

Query Match
50.0%; Score 2325; DB 1; Length 953;
Best Local Similarity 49.9%; Pred. No. 7.9e-112;
Matches 464; Conservative 175; Mismatches 264; Indels 26; Gaps

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13;

AKKSVDTVNQFLSLTQTG1AISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS 125 |: |: |: |: |: || || || || || || || 99

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A; Description: attacks blood cell membranes and causes cell lysis C; Superfamily: hemolysin A; hemolysin A homology C; Superfamily: hemolysin A; hemolysin A homology C; Keywords: calcium binding; cytolyais; exotoxin; hemolysis; lipoprotein; tandem repeat; F; 243-787/Domain: hemolysin A homology <HLYA>. F; 719-801/Region: 9-residue repeats (G-X-G-[DN]-D-X-[LVIYF]-X) F; 719-801/Region: 9-residue repeats (G-X-G-[DN]-B; 877/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIEASLITISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRLOGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: Lose
A; Molecule type: Lose
A; Molecule type: Lose
A; Cross-references: EMBL:XG1111; NID:g38939; PIDN:CAA43423.1; PID:g38941
A; Cross-references: EMBL:XG1111; NID:g38939; PIDN:CAA43423.1; PID:g38941
R; Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, Infect. Immun. S9, 4497-4504, 1991
Infect. Immun. S9, 4497-4504, 1991
A; Title: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A; Reference number: A43599; MUID:92040145; PMID:1937809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NSTKSGLKNLYLAIPKDYDPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSKITLSSLKSSLQOGLKNGKNKLNQAGTTLKNGLTQTGHSLQNGAKKLILYIPQGYDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIITGLLSGISAGFALADKWASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLST
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                A; Experimental source: serotype 5
R; Smits, M.A.; Briaire, J.; Jansen, R.; Smith, H.E.; Kamp, E.M.; Gielkens, submitted to the EMBL Data Library, July 1991.
A; Description: Cytolysins of Actinobacillus pleuropneumoniae serotype 9.
A; Reference number: $18852
A; Accession: $18853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASIDLINEIIGNLSOSTQTIEAFSSOLAKLGSTISQAKGFSNIGNKLONL-NFSKTNLGL
Cross-references: GB:M30602; NID:g141823; PIDN:AAA87232.1; PID:g141825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.1%; Score 2236.5; DB 1; Length 956; Best Local Similarity 47.7%; Pred. No. 2.8e-107; Matches 453; Conservative 188; Mismatches 255; Indels 53;
                                                                                                                                                                                                                                                                                                             A,Accession: B43599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-27;948-956 <SM2>
A;Cross-references: GB:X61111; NID:g38939
C;Comment: This organism causes porcine pleuropneumonia.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSNINV--IKSNIQAGL-------
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N;Alternate names: cytolysin II; RTX-toxin II (ApxII)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 09-Mar-1990 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: B33389; S18853; B43599
R;Chang, Y. P; Young, R.; Struck, D.K.
DNA 8, 635-647, 1989
A;Title: Cloning and characterization of a hemolysin gene from Actinobacillus A;Reference number: A33389; MUD:90126233; PMID:2693022
A;Molecule type: DNA
A;Residues: 1-956 <CHA>
                                                                                                                                                                                                                          GFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
                                                                                                                                                                                                                                                                                                                 HANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
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    AQTSLGTIQTAIGLTERGIVLSAPQIDKLLQK---TKAGQALGSAESIVQNANKAKTVLS 143
                                                                           GIQSILGSVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQISQ
                                                                                                                                                              FGSKLONIKGLGTLGDKLKNIGGLDKAGLGLDVISGLLSGATAALVLADKNASTAKKVGA
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F;745-753/Region: repeat
F;745-762/Region: repeat
F;747-762/Region: repeat
F;772-780/Region: repeat
F;732-780/Region: repeat
F;781-789/Region: repeat
F;8192-800/Region: repeat
F;8191-809/Region: repeat
F;801-809/Region: repeat
                                                                                                                                                                         DB 1; Length 955;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                       48.1%; Score 2236; DB 1; larity 48.2%; Pred. No. 3e-107; Conservative 178; Mismatches 271;
                                                                                                                                                                                                Local Similarity
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-955 < LAIS
A; Cross-references: EMBL: 226247; NID: 9400424; PIDN: CAB81206.1; PID: 9400425
R; Highlander, S.K.; Engler, M.J.; Weinstock, G.M.
J. Bacteriol. 172, 2343-2350, 1990
A; Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A; Reference number: A3524; MUID: 90236888; PMID: 2185213
A; Accession: A35254
A; Residues: 950-955 < HIG>
A; Cross-reference: BENA197; GB: M34943; GB: M34944
A; Residues: 950-955 < HIG>
A; Cross-reference: Dibrary. Unne 1993
A; Description: DNA sequence of the carboxy terminal end of leukotoxin A from the T3 sen
A; Reference number: S34235
A; Accession: S34237
A; Molcoule type: DNA
A; Residues: 745-955 < LA2>
A; Residues: 745-955 < LA2>
A; Residues: 745-955 < LA3>
A; Residues: 745-955 < LA3>
A; Residues: 723-955 < LA3>
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A; Residues: 724-955 < LA3>
A; Residues: Residue: Residue respeate (G-C-X-G-[DN]-D-X-[LVIYP]-X)
B; 718-725 / Residue: Respeate
B; 727-735 / Residue: Respeate
B; 727-735 / Residue: Respeate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukotoxin A - Pasteurella haemolytica (serotype T10)
NyAlternate names: lktA protein
C;Specias: Pasteurella haemolytica
C;Specias: Pasteurella haemolytica
C;Accession: 837145; A35254; S34235
C;Accession: 837145; A35254; S34237; S34235
R;Lainson, A.F.; Aitchison, K.; Donachie, W.
Bubmitted to the EMBL Data Library, September 1993
A;Description: DNA sequence of the leukotoxin A gene from P. haemolytica T10 serotype. A;Reference number: S37145
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                                          KSVEEVIGSOFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLL 745
                                                                                                                                                                                                  DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVK 805
                                                                                                                                                                                                                                                                               653 ATAETEKGSYSVKRYVGDSKALHETIATHQTNVGNREEKIEYR-REDDRFHTGYTVTDSL 711
                                                                                                                                                                                                                                                                                                                                       RNDHSGSINIPRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKD 861
                      -----ETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVD
                                                                                                GTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNL
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A, Molecule type: DNA
A; Residues: 1-1052 <JAN1>
A; Residues: 1-1052 <JAN1>
A; Residues: 1-1052 <JAN1>
A; Residues: 1-1052 <JAN1>
A; Cross-references: EMBL:X68815; NID:g38956; PIDN:CAA48711.1; PID:g38958
A; Cross-references: EMBL:X68815; NID:g38956; PIDN:CAA48711.1; PID:g38958
A; Experimental source: staracted from NCB1 backbone (NCBIN:125168, NCBIP:125170)
B; Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
B; Jansen, R.; Briaire, J.; van Geel, A.B.M.; Kamp, E.M.; Gielkens, A.L.J.; Smits, M.A.
A; Title: Genetic map of the Actinobacillus pleuropneumoniae RTX-toxin (Apx) operons: cha
A; Reference number: $48042; MUID:95012630; PMID:7927703
A; Accession: $48043
A; Accession: S48043
A; Accession: S48043
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C; Superfamily: hemolysin A; hemolysin A homology
C; Keywords: calcium binding; cytolysis; exotoxin; lipoprotein; tandem repeat; thiolester
F; 254-804/Domain: hemolysin A homology 
F; 736-862/Region: 9-residue repeats (G-3-X-G-[DN]-D-X-[LVIXF]-X)
F; 571,702/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin III - Actinobacillus pleuropneumoniae (serotype 8)
NyAlternate names: RTX-toxin III (ApxIIIA)
Cispeciaes: Actinobacillus pleuropneumoniae
Cispeciaes: Actinobacillus pleuropneumoniae
Cybate: 19-Dec-1993 #sequence revision 01-Nov-1996 #text_change 18-Jun-1999
CyAccession: B49219; A8043; Z2958
R;Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
Infect. Immun. 61, 947-254, 1993
A;Title: Cloning and characterization of the Actinobacillus pleuropneumoniae-RTX-toxin
A;Reference number: A49219; MUID:93162836; PMID:8432615
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Comment: This orgnism causes porcine pleuropneumonia.
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                                        AGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDG
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A,Residues: 1-1052 <JAN2>
A,Cross-references: EMBL:X80055; NID:9558150; PIDN:CAA56358.1; PID:9558152
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Matches 425; Conservative 166; Mismatches 287;
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C;Function:
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C;Species: Actinobacillus suis
C;Species: Actinobacillus suis
C;Species: Actinobacillus suis
C;Species: Actinobacillus suis
C;Species: Actinobacillus suis
C;Stecession: A43834
R;Burrows, L.L.; Lo, R.Y.
Infect. Immun. 60, 2166-2173, 1992
A;Tile: Molecular characterization of an RTX toxin determinant from Actinobacillus suis
A;Reference number: A43834; MUID:92267623; PMID:1587585
A;Reference number: A43834; MUID:92267623; PMID:1587585
A;Rolecule type: DNA
A;Residues: 1-956 cBUR>
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NKSOKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAPSV
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RTX toxin-III

1993 of the Actinobacillus pleuropneumoniae MUID:93263992; PMID:8494611

DNA Cell Biol. 12, 351-362, A,Title: Molecular analysis A,Reference number: S51783;

repeat; thiolester

21

Gaps

120;

Indels

Query Match 41.4%; Score 1924; DB 1; Best Local Similarity 43.0%; Pred. No. 3.8e-91; Matches 428; Conservative 152; Mismatches 296;

45 78

A,Accession: S51784
A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1049 < CHA>
A,Crose-references: EMBL:L12145; NID:g349605; PIDN:AAA21924.1; PID:g470685
C,Comment: This orgnism causes porcine pleuropneumonia.
C,Genetics:
A,Gene: apxIIIA
C,Function:
A,Description: lyses lung macrophages
C,Superfamily: hemolysin A; hemolysin A homology
C,Keywords: calcium binding: cytolysis; exotoxin; lipoprotein; tandem repeat; C,Keywords: calcium binding: cytolysis; exotoxin; lipoprotein; tandem repeat; F,254-803/Domain: hemolysin A homology <HLYA>
F,254-803/Domain: hemolysin A homology <HLYA>
F,351,702/Binding site: palmitate (Lys) (covalent) #status predicted

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                                                                                                                                                                                                                                                                                                                                               -- DLLDGGSGDDV 753
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KAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAK
                                   GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                                                                                           SGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAAL
                                                                                                                                                                                     TISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
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                                                                       IGNLSQSTQT1EAFSSQLAKLGST1SQAKGFSN1GNKLQNLN----FSKTNLGLE11TGLL
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-----NLYLAIPKDYDPQKGGTLNDFI
             KAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAK
                                                                                        GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEI
                                                                                                                                     IGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN---FSKTNLGLEIITGLL
                                                                                                                                                                                 SGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAAL
                                                                                                                                                                                                                              ITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLT
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551784
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Sin Actinobacillus pleuropneumoniae (seroty NyAlternate names: RTX-toxin IIIA (ApxIIIA)
C;Species: Actinobacillus pleuropneumoniae
C;Date: 14-Jul-1995 #sequence_revision 15-Nov-1996
C;Accession: Sin, J.; Ma, D.P.; Shin, S.J.; Lein,
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316

342 376 402 436 462 495 518 553 570 612 630 671 688 739

222 256 282

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A;Title: Fatty acylation of two internal lygine residues required for the toxic activity. A;Reference number: A5587; MUID:95099325; PMID:7801126
A;Reference number: A5587; MUID:95099325; PMID:7801126
A;Acortentes: amontation; lysine palmitoylation
A;Note: lysine modification is performed by the hlyC gene product
B;Haertlein, M.; Schiessl, S.; Wagner, W.; Rdest, U.; Kreft, J.; Goebel, W.
Cell Biol. 22, 87-97; 1983
A;Title: Transport of hemolysin by Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-1023 <FEL>
A,Cross-references: GB:M10133; GB:M12863; NID:g146377; PIDN:AAA23975.1; PID:g146379
A,Experimental source: strain J96, O4 serotype
A,Experimental source: Koronakis, V.; Hughes, C.
Science 266, 1992-1996, 1994
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                                                                                                                                                                                                                                                    KROETKVGKRIETIQYRDYELRKV-GYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFH 710
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GADGDDLIEGNDGNDRLYGDKGNDTLSGGNGDDQLYGGDGNDKLIGVAGNNYLNGGDGDD 801
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SRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADA 480
                                                                                                                                                                                                                                VGOGKMNIDGGDGHDRVFYSK-DGGFGNITVDGTSATEAGSYTVNRKVARGD--IYHEVV 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hemolysin A - Escherichia coli
C;Species: Escherichia coli
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 18-Jun-1999
                                                                                              FEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGK
                                                                                                                                                        YSYINKLKFGRVKNWQVTD-GEASSKLDFSKVIQRVAETEGT-DEIGLIVNAKAGNDDIF
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Bacteriol. 163, 94-105, 1985
A;Title: Nuclectide sequence of an Escherichia coli chromosomal hemolysin. A;Reference number: A24433; MUID:85234404; PMID:3891743
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A;Molecule type: DNA
A;Residues: 1,'T',3,'V',5,'T',7-44 <RES>
A;Cross-references: GB:M29173; NID:g146337; PIDN:AAA23957.1; PID:g146338
C;Genetics:
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$10056
hemolysin A - Escherichia coli plasmid pHly152
C;Species: Escherichia coli
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 04-Mar-2000
C;Accession: $10056
R;Hess, J; Wels, W.; Vogel, W.; Goebel, W.
FEMS Microbiol. Lett. 34, 1-11, 1986
R;Hess, J;Welsonideride sequence of a plasmid-encoded hemolysin determinant and its comparist A;Title: Nucleocide sequence of a plasmid-encoded hemolysin determinant and its comparist A;Reference number: $07209
A;Accession: $10056
A;Accession: $10056
A;Residues: 1-1024 <HES>
A;Censule type: DNA
A;Residues: 1-1024 <HES>
A;Geneme: plasmid pHly152
C;Genetics:
A;Genome: plasmid pHly152
C;Superfamily: hemolysin A; hemolysin A homology
C;Keywords: lipoprotein
F;247-792/Domain: hemolysin A homology <HEYA>
F;564,690/Binding site: palmitate (Lys) (covalent) #status predicted
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                                                                                                                    LNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVK--RND 808
                                                                                                                                          KSVDTVNQFLSLTQTGIAISATKLEKFLQKH--STNKLAKGLDSVENIDRKLGKASNVLS 125
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    EE-IGSNORDEFKGSKFRDIFHGADGDDLLNGNDGDDILYGDKGNDELRGDNGNDQLYGG 790
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leukocoxin A - Actinobacillus actinomycetemcomitans
[C.Species: Actinobacillus actinomycetemcomitans
[C.Species: Actinobacillus actinomyetemcomitans
[C.Joate: 16-Sep-1992 #sequence_revision 01-Nov-1996 #text change 31-Mar-2000
[C.Joate: 16-Sep-1992 #sequence_revision 01-Nov-1996 #text change 31-Mar-2000
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[S.Kraig, B.; Dailey, T.; Kolodrubetz, D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Analysis of the Actinobacillus actinomycetemcomitans leukotoxin gene. Delineatic A;Reference number: A34345; MUID:89359382; PMID:2670940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Residues: 1-239, Y', 241-259,'H', 261-335,'A',337-415,'S',417-438,'S',440-723,'N',725-926
PVKRYPLRHCRPIITLILIGIR' «LAL»
A,Cross-references: GB:M27933
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A;Title: Identification and expression of the Actinobacillus actinomycetemcomitans leukot A;Reference number: A32276; MUID:89165863; PMID:2647082
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A;Residues: 430-438,'S',440-476,'R',478-506,'RVRS',511,'QSIAINSLNTD',523-541,'I',543,'PQN
A;Note: this sequence is revised in reference A34345
R;Ohte, H.; Myagi, A.; Kato, K.; Fukui, K.
submitted to JIPID, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Keywords: cytolygis; hemolysis; lipoprotein; periplasmic space; tandem repeat; thioles F;245-790/Domain: hemolysin A homology <HLYA>
F;731-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actinomycetemo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A32276
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X16829; NID:g38643; PIDN:CAA34731.1; PID:g38645
A;Note: the authors present evidence that the nucleotide sequence is correct in
sing nucleotide
                             975
KESGDISNHQIEQIFDKDGRVITPDSLKKALEYQQSNNKASYVYGNDALAYGSQGNLNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinobacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;562,687/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1055;
                                                                                                                           911
                                                                                          --ELKKLADENKSQKLSASDIASSLNKLVGSMALFGTA-NSVSSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rixolodrubetz, D.; Dailey, T.; Ebersole, J.; Kraig, E. Infect. Immun. 57, 1465-1469, 1989
A;Title: Cloning and expression of the leukotoxin gene fakeference number: A60768; MUID:89212893; PMID:2707855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain 301-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.18;
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A;Residues: 2-6,'L',8-26 <OH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: PH0266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-1055 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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C;Function:
A;Pescription: attacks blood cell membranes and causes cell lysis
C;Superfamily: hemolysin A; hemolysin A homology
C;Superfamily: hemolysin A; hemolysis, exotoxin; hemolysis; lipoprotein; tandem repeat;
C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat;
E;246-791/Domain: hemolysin A homology <HLXA>
E;246-791/Domain: hemolysin A homology <HLXA>
F;723-851/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X)
F;563,689/Binding site: palmitate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420
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GADGDDHIEGNDGNDRLYGDKGNDTLSGGNGDDQLYGGDGNDKLIGGAGNNYLNGGDGDD 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         826 NYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKK------DGTVITSQ----- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSVDTVNQFLSLTQTGIAISATKLEKFLQKH--STNKLAKGLDSVENIDRKLGKASNVLS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFQNFLGTALSSMKIDELIKKQKSGGNVSSSELAKASIELINQLV-DTAASLMNVNSFSQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSS 181
                                                                                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                                                                                                                                                                                                                           KSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAK
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                             118;
                                                                                                                                                                                                                                            Length 1023;
                                                                                                                                                                                                                                                                         Best Local Similarity 41.8%; Pred. No. 4.2e-0/;
Matches 421; Conservative 156; Mismatches 311; Indels
                                                                                                                                                                                                                                                   Score 1845; DB 1;
Pred. No. 4.2e-87;
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                                                                    TETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ--KHSTNKLAKGLDSVENIDRKLGKA 120
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                                                                                                         SNVLSTLSSFLGTALAGIELDSLIK---KGDAAPDA-LAKASIDLINEIIGNLSQSTQTI 176
                                                                                                                                                                                                                        PLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVS 352
                                                                                                                                                                                                                                                               AGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQ 412
                                                                                                                                                                                                                                                                                                   NYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERIK 472
                                                                                                                                                                                                                                                                                                                                         SGKAYADAFEDGKKVEAGSN----ITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTES 528
                                                                                                                                                                                                                                                                                                                                                          SGKAYVDYLKKGEELAKHSDKFTKOILDPIKGNIDLSGIKGSTT--LTFLNPLLTAGKEE 554
                                                84
                                                                                                                                                                                   EAFSSQLAKLGSTISQAKGFSNIGNKLQNL----NFSKTNLGLEIITGLLSGISAGFALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNDVFHGHDGDDLIYGYDGDDRLYGDNGNDEIHGGQGNDKLYGGAGNDRLFGEYGNNYLD
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                              NINVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNH
           Indels 130;
   Pred. No. 1.4e-85; ; Mismatches 299;
40.2%; Fit-
            413; Conservative
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A;Residues: 1-1022 <RES>
A;Cross-references: EMBL:X73117; NID:g312897; PIDN:CAA51548.1; PID:g312899
R;Frey, J.; Malar, R.; Gygi, D.; Nicolet, J.
Infect. Immun. 59, 3026-3032, 1991
A;Title: Nucleotide sequence of the hemolysin I gene from Actinobacillus pleuropneumonia A;Reference number: S18769; MUID:91348845; PMID:1879928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residue=: 1-209,'AMPYLTLA',218-373,'R',375-561,'O',563-686,'TC',688-1022 cFRE>
A;Cross-terences: EMBL:X52899; NID:938949; PIDN:CAA37081.1; PID:938950
R;Frey, J; Haldimann, A.; Nicolet, J; Boffini, A.; Prentki, P.
Gene 142, 97-102, 1994
A;Title: Sequence analysis and transcription of the apxI operon (hemolysin I) from Actin A;Reference number: I39644; MUID:94237497; PMID:8181764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-209, AMPXILILA', 218-373, 'R',375-561,'Q',563-686,'TC',688-1022 <RE2>
A;Gross-references: EMBL:X68595; NID:9505568; PIDN:CAA48586.1; PID:9505570
A;Gross-references: EMBL:X68595; NID:961868; PIDN:CAA48586.1; PID:9505570
R;Tascon, R.I.; Vazquez-Boland, J.A.; Gutierrez-Martin, C.B.; Rodriguez-Barbosa, I.; Rod
Mc. Microbiol. 14, 207-216, 1994
A;Title: The RTX haemolysins ApxI and ApxII are major virulence factors of the swine pat:
A;Reference number: S60731; MUID:95131743; PMID:7830567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: attacks blood cell membranes and causes cell lysis C;Superfamily: hemolysin A; hemolysin A homology C;Superfamily: hemolysin A; hemolysin A homology C;Keywords: calcium binding; cytolysis; exotoxin; hemolysis; lipoprotein; tandem repeat; F;243-789/Domain: hemolysin A homology <HIXA>. F;721-847/Region: 9-residue repeats (G-G-X-G-[DN]-D-X-[LVIYF]-X) F;560,686/Binding site: palmitate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                          from GB/EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB/EMB
                         N;Alternate names: hemolysin ApxI
C;Species: Actinobacilus pleuropneumoniae
C;Date: 19-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 18-Jun-1999
C;Accession: 139643; S18769; T39645; S60732; S35781
R;Jansen, R.; Briaire, J.; Kamp, E.M.; Gielkens, A.L.; Smits, M.A.
Infect. Immun. 61, 3688-3695, 1993
A;Title: Structural analysis of the Actinobacillus pleuropneumoniae-RTX-toxin I (ApxI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1, Status: nucleic acid sequence not shown; translation not shown; translated from
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                                                                                                                                                                                                                                                                                                                                          ;Status: nucleic acid sequence not shown; translation not shown; translated
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C;Comment: This organism causes porcine pleuropneumonia
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RTX-toxin I - Actinobacillus pleuropneumoniae
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DNA Res. 5, 1-9, 1998

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DNA Res. 5, 1-9, 1998

DNA Res. 5, 1-9, 1998

DNA Res. 5, 1-9, 1998

A;Reference number: 214127; MUID:98290540; PMID:9628576

A;Accession: T00227

A;Accession: T00227

A;Accession: T00227

A;Residue: preliminary; translated from GB/EMBL/DDBJ

A;Residue: 1-998 cMAK>

A;Residues: 1-998 cMAK>

A;Residues: 1-998 cMAK>

A;Residues: L998 cMAK>

A;Residues: EMBL:AB011549; NID:94589740; PIDN:BAA31774.1; PID:93337015

A;Experimental source: strain EHEC O157:H7, substrain RIMD 0509952
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                                          S DADAGTKAAAGIEISTKILGNIGKAVSQYIIAQRVAAGLSTTAATGGLIGSVVALAISPL
                                                                      AFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAG
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large virulence plasmid of 126 SYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFV 595 610 742 GNDYIEGNYGNDRLYGDDGDDYISGGGDDQLFGGSGNDKLSGGDGNNYLTGGSGNDELQ 788 21 241 421 537 551 668 712 134 127 ISSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ 182 194 301 255 AAAGIELTTQVLGNVGKAVSQYILAQRMAQGLSTTAASAGLITSAVMLAISPLSFLAAAD 314 GQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGD--IYHEVVKR 653 KENHANALDEFAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTALGAVSAGVSAAAVG 361 RYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERIKSGKAYADAF 481 67 9/ | | | : | : | : | | | : | | | | : | | | | GAGSSEVFAGEGYDTVSYNKT-DVGKLTIDATGASKPGEYIVSKNM-YGDVKVLQEVVKG KSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL-DSVENIDRKLGKASNVLST VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD SAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDS KSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAK LAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKK EDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKY QETKVGKRTETIQYRDYELRKVGYGYGYDSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSG--------EGDDLLDGGAGDDRLFGGKGNDRLSGDEGD------Plunkett, G.; Sofia, H.J.; Blattner, R;Burland, V.; Shao, Y.; Perna, N.T.; Plunkett, G.; Sofia, H.J.; Blattner Nucleic Acids Res. 26, 4196-4204, 1998
A;Title: The complete DNA sequence and analysis of the large virulence pl A;Reference number: 222068; MUID:98391744; PMID:9722640
A;Recession: T42148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-998 cBUR>
A;Residues: 1-998 cBUR>
A;Residues: 1-998 cBUR>
A;Residues: 1-998 cBUR>
A;Cross-references: EMBL:AF074613; PIDN:AAC70116.1
A;Experimental source: strain BDL933; serotype O157:H7
C;Genetics:
A;Gene: hlyA
A;Gene: plasmid pO157
C;Superfamily: hemolysis A; hemolysin A homology
C;Keywords: cytolysis; hemolysis; lipoprotein; toxin
F;233-776/Domain: hemolysis; lipoprotein; toxin
F;250,675/Binding site: palmitate (Lys) (covalent) #status predicted 102; Indels 7.6%; Score 1748; DB 2; Local Similarity 40.0%; Pred. No. 3.9e-82; Nes 391; Conservative 177; Mismatches 308; 729 713 셤 8

Db 849 KGDRLHLSDISFDDIAFKRVGNDLIMUKAINGVLSFNESNDVNG-ITFKNWFAKD 902 Qy 828 QSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSOKLSASDI 887	Qy 538 SYINKLKFGRVKNMQYTDGEASSK-LiDFGKVLQRVAETEGTDEIGLINNAKAGNDDIFV 595 Db 552 EYMTSLIVNGKDTWSV-KÖITNINGTOYPSKLIQRVAETEGTDEIGLINNAKAGNDDIFV 595 Db 552 EYMTSLIVNGKDTWSV-KÖITNINGTOYPSKLIQRVENATKHYQARIISELGDKDDVVKR 653 Cy 596 GQGKMNIDGGDGHDRYFYSKDGGFGNITUDGTSATEAGSYTVNRKVARGD-IYHBVVKR 653 Ch 1 GAGSSEVPAGGGFTDPVSYNKT-DVGKLIJDATGAPKPGEYIVPKNM-YGDVEULQEVVKR 668 Cy 654 QETKVGKRTERIQYRDYELKRVGYGYOSTDNLKSSVEEVIGGFDNDFKGSKRNDIFHGAD 728 Ch 1
Query Match 37.2%; Score 1729; DB 2; Length 998; Best Local Similarity 39.8%; Pred. No. 3.78-81; Matches 102; Gaps 21; Matches 39.9%; Conservative 174; Mismatches 313; Indels 102; Gaps 21; Matches 39.0%; Conservative 174; Mismatches 313; Indels 102; Gaps 21; Oy KSNIQAGLMSTRGGLKALPENDPORGGTLNDFIKAADELEREPHTETAK 67 MENTALSSSVRAAGKLILLIDPDNYPAQ-CVGINELYKAADELGIEHRTERDDTALAN 76 Oy 6 KSVDTVNQFESITOTAISERTEREPROKTAKAGL DSVENIDERKLGKASNULST 126 SERICATALAGIELDSLIKKGDAAPDALAKASIDLINEIIGULSGSTQTIERFSSQ 182	RESULT 13 S15672 adenylate cyclase hemolysin - Bordetella bronchiseptica cippecises: Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Species Bordetella bronchiseptica C; Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999 C; Accession: S15672 Accession: S15672 A; Date a Library, September 1994 A; Residuate to the EMBL Data Library, September 1994 A; Residuate to the EMBL Data Library, September 1994 A; Residuate to the EMBL S1672 A; Residuate type: DNA A; Residuate type

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A;Residues: 1-1706 <GLA>
A;Residues: 1-1706 <GLA>
A;Residues: B;Cross-treferences: EMBL:Y00545; NID:g396665; PIDN:CAA68613.1; PID:g396666
B;Glaber, P.; Sakamoto, H.; Bellalou, J.; Ullmann, A.; Danchin, A.
EMBO J. 7, 3997-4004, 1988
A;Title: Secretion of cyclolysin, the calmodulin-sensitive adenylate cyclase--haemolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyclolysin - Bordetella pertussis

N'Alternate names: adenylate cyclase precursor; calmodulin-sensitive adenylate cyclase-h
N'Alternate names: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
N;Contains: adenylate cyclase (EC 4.6.1.1), calmodulin-sensitive; hemolysin
C;Species: Bordetella pertussis
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: 800893; 814100; 502389
R;Glaser, P.; Ladant, D.; Sezer, O.; Pichot, F.; Ullmann, A.; Danchin, A.
Mol. Microbiol. 2, 19-30, 1988
A;Title: The calmodulin-sensitive adenylate cyclase of Bordetella pertussis: cloning and A;Reference number: 800893; MUID:88216178; PMID:2897067
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TQKTAYGKRTENVQYRHVELARVGQ-LVEVDTLEHVQHIIGGAGNDSITGNAHDNFLAGG 1033
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                                                                                                                          YDSRYAAYLANN----LKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGK 475
                                                                                                                                                                                                                                                                            KYSYINKLKF-GRVKNWQVTDGEASSKLDFSKVIQRVAETEGT--DEIGLIVNAKAGNDD 592
                                                                                                                                                                                                                                                                                                                                   IFVGQGRMIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVK 652
                        AAGAEIALOLTGGTVELASSIALALAAARGVTSGLOVAGASAGAAAGALAAALSPMEIYG 624
                                                                                                                                                                                                                                     IVKRNDHSGSINIPRWY---ITSNLQNYQSNKTDHK-----IEQLIG---KDGSY
                                                                                                                                                                                                                     AYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNG
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                                                     AADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAA
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AAGFELSNQVIGNVTKAISSYVL-
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|IGDAQANTLMGQGGDDTV 1286
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A;Contents: annotation; identification of ademylate cyclase--hemolysin bifunctional prote R;Munier, H.; Gilles, A.M.; Glaser, P.; Krin, E.; Danchin, A.; Sarfati, R.; Barzu, O. Bur. J. Biochem. 196, 469-474, 1991

Bur. J. Biochem. 196, 469-474, 1991

A;Title: Isolation and characterization of catalytic and calmodulin-binding domains of B. A;Title: Isolation and characterization of catalytic and calmodulin-binding domains of B. A;Reference number: S14100

A;Reference number: S14100

A;Residues: 1-78, MY, 80, MY, 82-97, MY, 99-139, MY, 141-178, MY, 180-399 «MUN>

B;Residues: 1-78, MY, 80, MY, 82-97, MY, 99-139, MY, 141-178, MY, 180-399 «MUN>

A;Residues: 1-78, MY, 80, MY, 82-97, MY, 99-139, MY, 141-178, MY, 180-399 «MUN>

A;Reference number: A55167; MUID:95025937; PMID:79319682

A;Contents: annotation; lysine palmitoylation

C;Comment: B. pertussis, the etiological agent of whooping cough, disrupts mammalian cell action by host cell calmodulin of the ademylate cyclase activity of bacterial cyclolysin, C;Comment: Adenylate cyclase activity is activated upon binding of calmodulin in the vice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Superfamily: Cyclolysin; calmodulin-sensitive adenylate cyclase catalytic domain homolc (Keywords: Calcium binding; calmodulin binding; cAMP biosynthesis; carbon-oxygen lyase; F;15-328/Domain: calmodulin-sensitive adenylate cyclase catalytic domain homology cADE> F;25-35/Region: calmodulin binding #status predicted
F;59-66/Region: nucleotide binding #status predicted
F;54-1085/Domain: hemology cHLYA> F;411085/Domain: hemology cHLYA> F;411085/Domain: hemology cHLYA> F;103-1041,1042-1050,1174-1182,1289-1297,1298-1308,1316-1324,1430-1438,1556-1564/Region F;983/Binding site: palmitate (Lys) (covalent) #status experimental
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Reference number: S02386; MUID:89091151; PMID:2905265 Contents: annotation; identification of adenylate cycl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: cyaA; cya
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qq		Qy 320 GYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGAVGSAVGTPIALLVAGV 375
ò	724 DDRLFGGKG 732	Db 523 NQDGISQANELRTLEELGIQSLDLAYKDVNKNLGNGNTLAQQGSYTKTDGT 573
QQ	1046 NDTLVGGEGQNTVIGGAGDDVFLQDLGVWSNQLDGGAGVDTVKXNVHQPSEERLERMGDT 1105	Qy 376 TGLISGILEASKQAMFESVANRLQGKILEWEKQNGQNYFDKGYDSRYAAYLANNLKF 433
ò	733NDRLSGDEGDDLLDGGSGDDVLNG 756	Db 574 TAKMGDLILAADNLHSRFKDKVELTAEQAKAANLAGIGRLRDLREAAALSGDLAN 628
qq	1106 GIHADLQKGTVEKWPALNLFSVDHVKNIENLHGSRLNDRIAGDDQDNELWGHDGNDTIRG 1165	Cy 434 LSELNKELEA-ERVIAITQORWDNNIGELAGITKLGERI- 471
à	757 GAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSG 811	Db 629 MLKAYSAAETKEAQLALLDNLIHKWAETDSNWGKKSPWRLSTDWTQTANEGIALTPSQVA 688
qq	1166 RGGDDILRGGLGLDTLYGEDGNDIFLQDDETVSDDIDGGAGLDTVDYSAMIHPG 1219	OY 472KSGKAYADAFEDGKKVEAGSNITLDAKTGIIDI 504
à	812 SINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKI 855	Db 689 QLKKNALVSLSDKAKAAIDAARDRIAVLDAYTGQDSNTLYYMSEEDALNIVKV 741
eg G	1220 RIVAPHEYGFGIEADLSREWVRKASALGVDYYDNVRNVENVIGTSMKD-VLIGDAQANTL 1278	Qy 505 SNSNGKKTQALHFTSPLLTAGTESRERLTNG 535
ò	856 LQDKKDGTV 864	Db 742 TNDTYDHLAKNIYQNLLFQTRLQPYLNQISFKMENDTFTLDF-SGLVQAFNHVKETNP 798
ф	1279 MGQGGDDTV 1287	Qy 536 KYSYINKLKFGRVKNWQVTDGEASSKL-DFSKVIQRVAETEGT 577
6 11000		DD 799 QKAFVDLAEMLAYGELRSWYEGRRLMTDYVEEAKKAGKFEDYQKVLGQETVALLAKTSGT 858
E81086 iron-re C;Speci	ıs egulated protein FrpC NWB1415 [imported] - Neisseria meningitidis (strain MC58 ser ies: Neisseria meningitidis	QY 578 DEIGLIVNAKAGNDDIFVQQGKMNIDGGDGHDRVFYSKDGGFGNITV- 624
C; Date C; Acce	: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 ssion: E81086	Qy 625DGTSATEAGSY-TVNRKVARGDIYHEVVKRQETKVGKRTE 663
R, Tette Hickey,		
Science	; Oln, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. e 287, 1809-1815, 2000 Grae, Grandi G., Sun, I., Smith H.O., Bracar C.M., Moxon R.B., Banmioli, R., Ve	OY 664 TIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSK 704
A; Title	strain MC58.	Db 977 EIHFDNGKVLDVATVKELVQQSTDGSDRLYAYQSGNTLNGGLGDDYLYGADGDDLLNGDA 1036
A; Acces A; Stati A; Molec	A;Accession: E81086 A;Status: preliminary A;Molecule type: DNA	QY 705 FNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLN 755 :
A; Resid A; Cross A; Exper C; Genet	A;Residues: 1-1829 <tet> A;Cross-references: GB:AE002490; GB:AE002098; NID:g7226651; PIDN:AAF41776.1; PID:g722665 A;Experimental source: serogroup B, strain MC58 C;Genetics:</tet>	Qy 756 GGAGNDVXIFRKGDGNDTLYDGTG-NDKLAFADANISDIMIERTKEGIIVKRNDH 809 : : :
A;Gene:		Qy 810 SGSINIPRWYITSNLONYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQE 869
Quer. Best Matcl	Query Match 9.4%; Score 43/; DB 2; Length 1829; Best Local Similarity 20.4%; Pred. No. 2.4e-14; Matches 227; Conservative 175; Mismatches 365; Indels 346; Gaps 46;	1156 SGQVTVQYYFQNDGSGAYRIDEIHFDNGKVLDVATVK
& 43	IKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGI) 	Qy 870 LKKLADENKSQKLSASDIASSLNKLVGSMALFG 902
ò	AKKSUDTUN-QFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNUL	RESULT 16 835027
<u>a</u> 8	275DDLNTQWNNLTQAABIIYNDIVDNTSQGIBKGVKAIKELSBKMKNAASDL 324	Cytotoxin RTX homolog irpC - NeisBeria meningitidis C;Species: Neisseria meningitidis C.nata. 03-Beh-1904 #semmane ravision 03-Beh-1904 #text change 08-Oct-1999
· 영국	A	,
ò	185 KGFSNIG 200	MOI. MICTODIOI. 9, 85-76, 1393 AyItle: Cloning and nucleotide sequence of frpC, a second gene from Neisseria meningiti A;Reference number: S15026; MUID:94018616; PMID:8412674
qq		A,Accession: S35027 A,Molecule type: DNA
දු පු	201 NK-LONLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKA 259	A;Residues: 1-1829 <tho> A;Cross-references: GB:L06299; NID:g293961; PIDN:AAA99902.1; PID:g293963 C;Genetics:</tho>
& 8	260 ISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKF 319	Ajoene: Lipu Query Match Best Local Similarity 21.9%; Pred. No. 3e-14;

Matches	231; Conservative 167; Mismatches 355; Indels 302; Gaps 48;	
ò	43 DPIKAĄDELGIARLAEEPNHTETAKKSVDTVNOPLSLTQTGIALSATKLEKF 94	RESU
QQ Q	478 DNIKLADGSFAKHGYAALAELDSNGDNINAADAAFQTLRVWQDLNQDGIS 528	iron
è	95 LOKHSTNKLAK-GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGD- 148	and; and; and;
qq	529 -QANELRILEELGIQSLDLAYKDVNKNLGN-GMTLAQQGSYTKTDGTTAKMGDLLLAADN 586	A, Te
È	149AAPDALAKASIDLINBIIGNLSQSTQTIEAFSSQLAKL 186	r r r
qq	587 LHSRFKDKVELTÄEQAKAANLAGIGRLRDIREAAALSGDLANMIKAYSAAETKEAQLALL 646	A; Au
ò	187 GSTISQ-AKGFSNIGNKIQNLNFSKT-NLGLEIITGLLSGISAGFALADK 234	A;Re
qq	647 DNLIHKWAETDSNWGKKSPWRLSTDWTQTANEGIALTPSQVAQLKKNALVSLSDKAKAAI 706	A;St
È	235NASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAAL 282	A;Re
qq	707 DAARDRIAVLDAYTGQDSSTLYYMSEEDALNIVKVTNDTYDHLAKNIYQNLL 758	A S
ò	283 ITSSIMIAISPLAFMNAADKFNHANALDEFAKOFRKFGY 321	A. Ge
Q Q	759 FQTRLQPYLNQISFKMENDTFTLDFSGLVQAFNHVKETNPQKAFVDLAEMLAYGELRSWY 818	28
ò	322 DGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAVGTPIALLVA 373	Wa
qq	819 EGRRIMADIYVEEAKKAGKFEDYQKVLGQETVALLAKTSGTQADDILQNVGFGHNKNVSLY 878	δ
ò	374GVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNY-FDKGYDSRY 423	qq
qq	879 GNDGNDTLIGGAGNDYLEGGSGSDTYVFGKGFGQDTVYNYDY 920	ò
ò	424 AAYLANNLKFLSELNKELEAERVIAITQQRWDNNIG 459	qa
qq	921 ATGRKDIIRFTDGITADMLTFTREGNHLLIKAKDDSGQVTVQSYFQNDGSGAYRIDEIHF 980	ò
ò	460SLAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIID 503	qq
Dp	981 DNGKVLDVATVKELVQQSTDGSDRLYAYQSGNTLNGGLGDDYLYGADGDDLLNGDAGNDS 1040	ò
ò	504 ISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLD 563	qq
Db 1	1041 IYSGNGNDTLNGGEGNDALYGYNGNDALNGG 1071	ò
ò	564 FSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMIDGGDGHDRVFYSKDGGFGNIT 623	q _O
c qq	1072EGNDHLNGEDGNDTLIGGAGNDYLEGGSGSDTYVFGKGFGQDT 1114	ò
ò	624 VDGTSATEAGSY-TVNRKVARGDIYHEVVKRQETKVGKR 661	q 0
c qa	1115 VYNYDYATGRKDIIRFTDGITADMLIFTREGNHLLIKAKDGSGQVTVQSYFQNDGSGAYR 1174	ò
ò	662 TETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKG 702	QQ
c qa	1175 IDEIHFDNGKVLDVATVKELVQQSTDGSDRLYAYQSGNTLNGGLGDDYLYGADGDDLLNG 1234	ò
ć	703 SKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDV 753	qq
c qo	1235 DAGNDSIYSGNGNDTLDGGEGGNDALYGYNGNDALNGGEGNDHLNGEDGNDTLIGGAGNDY 1294	ò
È	754 INGGAGNDVYIFRKGDGNDTLYDGTG-NDKLAFADANISDIMIERTKEGIIVKRN 807	qq
qq	TYVFGKGFGQDT	ò
ò	808 DHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITS 867	අ <u>ය</u>
qq	1354 DDSGQVTVQSYFQNDGSGAYRIDEIHFDNGKVLDVATVKELVQQSTDG 1401	ò
ò	868 QELKKLADENKSQKLSASDIASSLNKLVGSMALFG 902	qu
qq	1402SDRLYAYQSGSTLNGGLGDDYLYG 1425	ò

n-regulated protein FrpA, probable NMB0585 [imported] - Neisseria meningitidis (strair pecies: Neisseria meningitidis ate: 31-Mar-2000 #text_change 19-Jan-2001 Accession: Called Mondards, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. ckey, E.K.; Haft, D.H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. ckey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; H.; A.; My Yomatheran, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. anthors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

Reference number: A81000; MUID:20175755; PMID:10710307 Status: preliminary Wolecule type: DNA Residues: 1-1302 <TET> Status Freferences: GB:AE002414; GB:AE002098; NID:g7225809; PIDN:AAF41013.1; PID:g722581/ Styperimental source: serogroup B, strain MC58 200 341 444 369 ALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKONGGONYFDKG--YDSRYAAY 426 |: :| : : | | :| | 495 LSGDLANMEKAYSAAETKEAQLALLDNLIHKWAETDSNWGKKSPMRLSTDWTQTANEGIA 554 571 VAETEGTDEIGLIVN-----AKAGNDDIFVGQGKWNIDGGDGHDRVFYSKDGG 618 313 AKQFRKFGYDG----DHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAVGSAVGTPI 368 ------41T 465 555 LTPSQVAQLKKNALVSLSDKAKAAIDAARDRIAV-----LDAYTGQDSNTLYYMSEED 607 608 ALNIVKVTNDTYDHLAKNIYQNLLFQTRLQPYLNQISFKMENDTFTLDF-SGLVQAFNHV 666 619 FGNITV-------DGTSA----TEAGSY-TVNRKVARGDIYHEVVKRQET 656 ----YGYQSTDNLK---SVEEVIGSQFN 697 | : | : : : | : : : | : : : | : 843 SGAYRIDEIHFDNGKVLDVATVKELVQQSTDGSDRLYAYQGSGNTLNGGLGDDYLYGADGD 902 698 DVFKGSKFNDIFHSGEGDDLLDGGAGDDRLF------GGKGNDRLSGDEGDDLLDGG 748 529 RERLINGKYSYIN---KLKFGRVKNW------QVTDGEASSKL-DFSKVIQR----193 AKGFSNIGNKLONLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFELSNQV ------GNGI 253 IGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDEF 466 KLGERI------KSGKAYADAFEDGKKVEAGSNITLDAKTG--------GKKTQALHFTSPLLTAGTES uery Match 9.1%; Score 421; DB 2; Length 1302; lest Local Similarity 22.5%; Pred. No. 9.6e-14; atches 198; Conservative 136; Mismatches 292; Indels 254; Gaps 427 LANNLKFLSELNKELEA-ERVIAITQ---QRW---DNNIGELA----303 AKGPS-----GSLFDHTNNGIRTATGWVSA-DDGLLVRDLN--657 KVGKRTETIQYRDYELRKVG-----501 ---IIDISNSN---- 105 ene: NMB0585

306 ANALDEPAKQFRKFGYDGDHILLAEYQRGVGTIBAS 1033 DTIEGGGTDKLVFGEGILAADVRLIREGQDVVLDLGNGHDSIRLKDWLTSNGTRNHSAD 341 LTTISTALGAVSAGVSAAAVG-SAVGTPIALLVAGVTGLISGILEASKQAMFE 1093 IEQIV	1931NOGDGHDTTIEGOGTDKLVFGEGILAA	RESULT 19 C82779 hemolysin-type calcium binding protein XF0668 [imported] - Xylella fastidiosa (strain 9a C;5pecies: Xylella fastidiosa C;5pecies: Xylella fastidiosa C;5pecies: Xylella fastidiosa C;5pecies: Xylella fastidiosa C;5pecies: Xylella fastidiosa C;5pecies: Xylella fastidiosa C;5pecies: C82779 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentary R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequentary R;anonymous, The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1208 <sim>A;Acsidues: 1-1208 <sim 1-1200="" 1-1208="" 1-1209="" <sim="" a;acsidues:="" a;actues:="" a;residues:="" a<="" th=""></sim></sim>
	RESULT 18 B82736 B82736 Comparison binding protein XF1011 [imported] - Xylella fastidiosa (strain 98 c) Species: Xylela fastidiosa Comparison B82736 Comparison	Query Match 8.9%; Score 415; DB 2; Length 1636; Best Local Similarity 22.4%; Pred. No. 2.7e-13; Matches 226; Conservative 150; Mismatches 323; Indels 308; Gaps 48; Qy 25 LYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQ 81 Db 793 MYLALPPRQLSAFTDAFABAYAKLKESIYIRLVLEPRLTDYLSGLLTD QY 82 TG-IAISATKLEKLQKHSTTNKLAKESIYIRLVLEPRLTDVLSGAASGWK 889 Db 842 NGWAAWDASGLEAKLDGTWQHNKAQALQDVMDLYRYGSNAVAASGWK 889 QY 140LDSLIKKGDAAPDALAKASIDLINBIGNLSQSTQTIEAFSSQLAKLGSTISQ 192 Db 890 PFDALRHMIDRTAATPDGRQALAAAEITLVSGNAEGSDAADLLFGDAGANLLR 942 QY 193 AKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAAGFE 247 Db 943 GGG

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----GITKLGERI-------KSGKAYADAFEDGKKVEA 489
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chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M., de Rosa Jr., V.E.; de Sa. R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A;Contents: annotation
C;Genetics:
A;Gene: XF0668
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                                                                                                                           Query Match 8.8%; Score 411; DB 2; Length 1208; Best Local Similarity 22.0%; Pred. No. 2.8e-13; Matches 227; Conservative 169; Mismatches 344; Indels 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGGEDYIGRGISEWGELLEKWYKQDFLPYLEKEWDQFPKFEDWLPEFPEWAREWLKLDPK 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILE 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferregulated RTX cytotoxin homolog FrpA - Neisseria meningitidis
C;Species: Naisseria meningitidis
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: A47058
R;Thompson, S.A.; Wang, L.L.; West, A.; Sparling, P.F.
J. Bacteriol. 175, 811-818, 1993
A;Title: Neisseria meningitidis produces iron-regulated proteins related to the A;Reference number: A47058; MUID:93139051; PMID:8423153
A;Contents: FAM20
A;Accession: A47058
A;Accession: A47058
A;Residues: preliminary
A;Residues: 1-1115 < THO>
A;Residues: 1-1115 < THO>
A;Note: sequence extracted from NCBI backbone (NCBIN:123557, NCBIP:123558)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGTALA--GIEL--DSLIKKGDAAPDALAK--ASIDLINEIIGNLSOSTQTIEAFSSQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 LLVRDLN-----GNGIIDNGAELFGDNT---KLADGSFAKHGYAALAELD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IAISA-----TKLEKFLQ-KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSGKYHVYDPLALDLDGDGIETVAAKGFA-----GALFDHRNQGIRTATGWVSA-DDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDTLKGWQGKDILLGGDGDDVLDGGEGSNRLEGGAGNDVLKVSYWSADNVLIGGTGDDTL
                                                           NGGAGNDVY1FRKGDGNDTLYDGTGNDKLAFADA-N1SD1M1ERTKEG11VKRNDHSGS1
                                                                                         814 NIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 AIGDIFIAAGDGLQYIKQQTEAMAQSKFLPTKLKTGLNDV--LNSRMLKSSTVLQHELNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --AKGFSNIGNKLONLNFSKTNLGLEIITGLLSGISAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAISPLAFMNAADKFNHANALDEFAKQFRKFGYDG----DHLLAEYQRGVGTIEASLTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNLG---NGNTLAQQGSYTKTD----GTTAKMGDLLLAA-----DNLHSRPKDKVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEKONGGONYFDKG--YDSRYAAYLANNLKFLSELNKELEA-ERVIAITQ---ORW---D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNOFLSL-----TQTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K----LGST1SQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 408.5; DB 2;
Local Similarity 20.4%; Pred. No. 3.4e-13;
les 239; Conservative 171; Mismatches 364;
                                                                                                                                                                                                                                                                                                                        | :| :| |
| CDHKESPRLVASSI 1207
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fami]

nnce number: A59328 tts: annotation cs: XF2407 Match Match	Similarity 25.4%; Pred. No. 6.5e-12; 5; Conservative 89; Mismatches 163; Indel VIAITQORWDNNIGELAGITKLGERIKSGKAYADAFEDGKK-	Db 1588 VLKVAYRSADNVLIGGTGDDTLYGSAYADTYLFNKGDGHDTITEQGGDDTLVFGA 1 Qy 500 GIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEAS 5	Db 1643 GIVRVLREGQDVVLDLGNGHBSIRLKDWLTSDGYRN 1 OY 560 SKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHPRVF 6	Db 1683 GNNDIEQIVFADGTIWTPETLSSMGLTTLGTSGNDTLKGWQGKDILLGGBGDDVL- 1 Oy 613 YSKDGGFGNITVDGTSATEAGSYTVNRKVARGD 6	Db 1738DGGMGSNRLEGGAGNDVLKVAYRSADNVLIGGTGDDTLYGGYADTYLFNKGD 1	Db 1791 GHDTIIEQGGDDTLVFGAGIVASQVRVLREGQDVVLDLGNGHDSIRLKDWLTSDGYR 1 Qy 681 STDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGGDDLLDG 7	-6 5	Db 1906 GMGSNRLEGGAGNDVLKVAXRSADNVLIGGTGDDTLYGSAYADTYLFNKGDGHDTIIEQG 1 Qy 779 GNDKLAPDANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKI 8	1966 GDDTLVFG-AGLHQKEARFTKSGNDLSILFNASEDQVTIAGWF	PB 2015 ESLVFQÖGT-VLSGEVERLIAAMALSSAVTTTQ-ASVRÖTKESHRİVÄSSİ 2063 834328 194328 1940ctoxin A - Pasteurella haemolytica (fragment) N;Alternate names: lktA protein C;Species: Pasteurella haemolytica C;Baccise: Pasteurella haemolytica C;Accession: S34238; S34236 R;Jainson, AF.; Aitchison, K.D.; Donachie, W. submitted to the EMBL Data Library, June 1995 #text_change 23-Mar-2001 C;Accession: S34238, S34236 A;Description: DNA sequence of the carboxy terminal end of leukotoxin A from of Pasturella haemolytica. A;Description: DNA sequence of the carboxy terminal end of leukotoxin A from of Pasturella haemolytica. A;Accession: S34236 A;Accession: S34236 A;Accession: S34236 A;Residues: 1-208 «LAD.) A;Residues: 1-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 9-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 2-208 «LAD.) A;Residues: 3-208 «LAD.)
	509GKKTQALHFTSPLLTAGTESRETTNGKYSYINKLKFGRVKWWQ	Qy 553 VTDGEASSKL-DFSKVIQRVAETEGTDEIGLIVNAKAGNDDIF 594 ::: : :: : : : : Db 714 VEEAKKAGKFEDYQKVLGQETVALLAKTSGTQADDILQNVGFGHNKNVSLYGNDGNDTLI 773	QY 595 VGQKMNIDGGBGHDRVFYSKDGGFGNITVDGTSATEAG 633	QY 634 SY-TVNRKVARGDIYHEVVKRQETKVGKRIETIQYRDYELRKVG	Qy 677 YGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLF 728	Qy 729GGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGND 781	Qy 782 KLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIG 841 :	Qy 842 KDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSM 898	Qy 899 ALFGTANSVSSNALQPITQPTQGILAPS 926 	RESULT 21 Ga2562 Dacteriocin XF2407 [imported] - Xylella fastidiosa (strain 9a5c) C.Species: Xylella fastidiosa C.Becteriocin Ga2562 R.Species: Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 15-157, 2000 A.Title: The genome sequence of the plant pathogen Xylella fastidiosa. A.Recession: Ga2552 A.MUD:2036517; PMID:10910347 A.Recession: Ga2562 A.MOCLESION: Gauthors see reference number A59328 below A.Reference number: A82515; MUID:20365717; PMID:10910347 A.Residues: Dreliminary A.Residues: Dreliminary A.Residues: T.2064 ASIMA A.Residues: T.2064 ASIMA A.Residues: GBAE004049; GB:AE003849; NID:g9107579; FIDN:AAF85206.1; GSPDB:GN001 A.Gross-references: GBAE00409; GB:AE003849; NID:g9107579; FIDN:AAF85206.1; GSPDB:GN001 A.Status: Dreliminary A.Residues: C.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asimpson, A.J.G.; Reinach, R.C.; F. Endargo, L.E.A.; Garraro, A.J.G. A.Gross-references: GBAE004049; GB:AE003849; NID:g9107579; FIDN:AAF85206.1; GSPDB:GN001 A.Burinest Lerences: GBAE00409; GB:AE003849; NID:g9107579; FIDN:AAF85206.1; GSPDB:GN001 A.Burinest Lerences: GBAE00409; GB:AE003849; NID:g9107579; FIDN:AAR86206.1; GSPDB:GN001 A.Burinest Lerences: GBAE00409; GB:AE003849; NID:g9107579; Former, A.J.G. B.; Submoon, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, A.J.G. B.; Junqueira, M.L.; Kemper, B.L.; Krajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laigt C., Branco, M.A.; Madeira, A.M.B.N.; Madeira, H.F.; Marcukuma, A.Y.; Menck, C.F.M.; Marcuca, B.C.; Mayaki, C.Y.; A.Authors: Martins, B.M.F.; Mateukuma, A.Y.; Menck, C.F.M.; Marcuca, B.C.; Mayaki, C.Y.; FANGON, C.F., F. G.; Numse, L.E., Marcukuma, A.Y.; Menck, C.F.M.; Marcuca, B.C.; Mayaki, C.Y.; F. G.; Numse, L.E., Marcukuma, A.Y.; Menck, C.F.M.; Marcuca, B.C.; Mayaki, C.Y.; F. G.; Numse, L.E., Marcukuma, A.Y.; Menck, C.F.M.; Marcukuma, A.J. de M.; de M.; de Soa J.V., VE.S.; R. G.; Santelli, R. W.; Rauthors: da Silva, M.F.; Versea, A.J. de M.; de M.; de Soa Silva, Versea, Versea, A.J., de M.; de M.; de M.; de

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1; DB 2; Length 2064;
. 6.5e-12;
tches 163; Indels 144; Gaps 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLDLGNGHDSI------RLKDWLTSDGYRN 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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| ::|::|::||
| REGODVVLDLGNGHDSIRLKDW---LTSDGYR 1847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKAYADAF----EDGKK--VEAGSNITLDAKT 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRERLTNGKYSYINKLKFGRVKNWOVTDGEAS 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVF 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NITVDGT-----SATEAGSYTVNRKVARGD 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGT 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRNDHSGSINIPRWYITSNLQNYQSNKTDHKI 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITSQELKKLADENKSQKLSASDI 887
:|:::|:|:|:|:|:|||
VTTTQ-ASVRDTKESHRLVASSI 2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agment)
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, W. 993 terminal end of leukotoxin A from the T4 serc

mology otoxin; hemolysis; lipoprotein; tandem repeat

Query Match 8.2%; Score 383; DB 2; Length 208; Best Local Similarity 37.8%; Pred. No. 6.1e-13; Matches 79; Conservative 52; Mismatches 64; Indels 14; Gaps 8;	QY 455 DNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKKTQA 514
Qy 723 GDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLAGGAGNDVYIFRKGDGNDTLYDGTGNDK 782 :	Qy 515 LHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAET 574 Db 323VSGTQADDILQNVGFGHNRNVSL 345
Qy 783 LAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQ 838 : : : : : : : : : : : : : : : : : : :	Qy 575 EGTDEIGLIVNAKAGNDDIFVGGGRANIDGGDGHDRVFXSKDGGFGNITV 624
Qy 839 LIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDIASSLNKLVGSM 898	Qy 625DGTSATEAGSY-TVNRKVARGDIXHEVVKRQETKVGKRTETIQYRDYEL 672 BD 394 DIIRFTDGITADMLTFTREGNHLLIKAKDDSGQVTVQSYFQNDGSGAYRIDEIHFDNGKV 453
Qy 899 ALFGTANSVSSNALQPITQPTQGILAPSV 927 :	Qy 673 RKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGE 713
RESULT 23 F81856 probable RTX-family exoprotein NMA1626 [imported] - Neisseria meningitidis (strain Z2491 C;Species: Neisseria meningitidis C;Date: 05-May_2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001	114 GDDLLDGGAGDDRLFGCKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY
R.Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 202-506, 2000 Nature 404, 2000 Arithe: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.	822 SNLONYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQK 633 EN
A;Reference number: A81775; MUID:2022556; PMID:10761919 A;Accassion: F81856 A;Status: preliminary A;Molecule type: DNA	Qy 882 LSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGILAPS 926
A;Residues: 1-697 <par> A;Residues: 1-697 <par> A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84854.1; PID:g738026 A;Experimental source: serogroup A, strain Z2491 C;Genetics: A;Gene: NWA1626</par></par>	RESULT 24 AH2515 hypothetical protein alr7304 [imported] - Nostoc sp.: (strain PCC 7120) plasmid pCC7120al
Query Match 7.9%; Score 366; DB 2; Length 697; Best Local Similarity 21.1%; Pred. No. 2.6e-11; Matches 201; Conservative 130; Mismatches 294; Indels 328; Gaps 37;	A.Note: Nostoc pp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AH2615
Qy 45 IKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ 96 :::	Rikaneko, 1.; Nakamura, 1.; Wolk, C.F.; Kuritz, 1.; Sasamoto, S.; Warumabe, M.; Ingumin, D. Bringuchi, M.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001 A. A. Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
Qy 97 KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK 156	A; Accession: AH2515 A; Accession: AH2515 A; Molecule type: DNA
Qy 157 ASIDLINBIIGNLSQSTQTIEAFSSQLAKLGSTISQ-AKGFSNIGNKLQNLNFSKTNLGL 215	A/Cross-references: GB:BA000020; PIDN:BAB78388.1; PID:g17135842; GSPDB:GN00180 A/Experimental source: strain PCC 7120 C/Genetics:
Qy 216 EIITGLLSGISAGPALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQ-RVAAGLS 274 :	A,Genome: plasmid A,Genome: plasmid Query Match 7.4%; Score 344; DB 2; Length 4936;
Qy 275 TTGAVAALITSSIMLAISPLAFMANAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGV 334	Best Local Similarity 22.1%; Fred. No. 86-09; Matches 233; Conservative 133; Mismatches 360; Indels 330; Gaps 48; Qy 24 NLYLAIPKDYDPQKGGTLNDPIKAADELGIARLAEEPNHTETAKKSVDT 72
Oy 335 GTIEASLTTISTALGAVSAQVSAAQCSAVGTPIALLVAGVTGLISGILEASKQAMFESV 394	Db 3662 NSDIIVLKVFKDNGAGSFADLEKALQWVAANSNTYNIASVNLSIGDSQNWT-TATGRYGI 3720
Db 229TRLQPYLNQISFKMENDTFTLDFSGLVQAFNHVKETNPQKAFVDL 273 OV 395 ANRLOGKTLEWEKONGGONYFDKGYDSRYAANNLKFLSELNKELEAERVIAITOORW 454	QY 73 VNQFLSLTQTGIALSATKLEKFLQKHSTNKLAKGLDSVENIDRKLGK 119 :::: :
274	

8 6 8 6 8 6 8	180 SEQLAKLGSTISQAKGFSNIGNKL	A;Autho Ster, E A;Title A;Acfer A;Setu A;Molec A;Cross A;Cross A;Cross A;Cross A;Gene: A;Gene:	A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W. A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Reference number: AB2577; MUID:21608550; PMID:11743193 A; Accession: AH3098 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1944 <kur> A; Residues: 1-1944 <kur> A; Residues: 1-1944 <kur> A; Residues: 1-1944 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur> A; Residues: 1-1044 <kur 1-1044="" 1-1<="" <kur="" a;="" residues:="" th=""></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur></kur>
දු පු	311EFAKQFRKP-GYDGDHLLABYQRGVGT1EASLTTISTALGAVSAGVSA 357	Query Best Match	Query Match 7.1%; Score 330.5; DB 2; Length 1944; Best Local Similarity 21.7%; Pred. No. 7.7e-09; Matches 218; Conservative 147; Mismatches 333; Indels 305; Gaps 48;
& g	358 AAVGSAVGTPIALLVAGVTGL-ISGILEASKQAMPESVANRLQGKILEWEKQNG 410 : :-	y da	66 AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHST-NKLAKGLDSVENI 113 : : : : :
& 8	411 GQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIALTQQRWDNNIGELAGITKLGER 470	vo ad	114 DRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNL 169
& g	471 IKSGKAYADAFEDGKKVEAGS-NITLDAKTGIIDISNSNGKKTQALHFTSPL 521 : : : : : 4119NVDVGTLNITVQAIDTSNASISDSFVLTITNLINNIVGTSG 4159	λō ;	170 SQSTQTIEAFSSQLAKLGSTISQAKGFSNIGN-KLQNLNFSKTNLGLEIITGLLISG 224 :: :
& g	522LTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDF 564	yo, da	225 ISA-GFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALI 283 :
상 음	565 SKVIQRVAETEGTDEIGLI	λ _O	284 TSSIMLAISPLAFMNAADKFNHANALDEFAKÇFRKFGYDGDHLLAEYQRGYGTIEAS 340
ራ 8	586 AKAGNDDIFVGQ-GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARG 644	λ _O q _O	341 LTTISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQA 389 :
\$ 8	645 DIXHEVVKRQETKVGKRTETIQYRDYELRKVG-YGYQSTDN-LKSVEEVI 692	ζο Op	390 -MFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIA 448 : :::
yo d	693 GSQFNDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDD 752 	, do	449 ITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKKVEAGSN 492
ò a	753 VLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGS 812	Qy	493ITLDAKTGIIDISNSNGKKTQALHFTSP 520 :
රු සි	813 INIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKK 872 	Qy	521 LL-TAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSK 566 1074 LLQTTGLMSRELTWNGAINSDKYKRGWSPMGDGVNVLRLGTVALFNDPAAQAWTDYA- 1130
රු සි	873 LADENKSQKLSASDIASSLNKLVGSMALFGTANSVS 908 1	yo da	567 VIORVAETEGTDEIGLIVNAKAGNDDIFVGQGRANIDGGDGHDRVFYSKDGGFGNI 622
RESULT AH3098 rhizobi C;Speci C;Date: C;Acce R;Wcce R;Wcce R;Karp,	AH30DLT 25 AH30Diocin/RTX toxin [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: AH3098 E;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001	8 8 8 8 8	623TVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVG 676 1182 RMKNGIEEILAQVPGKYEPGGEMKLRVEVIGDKITAFLNEEALFAYPIGDRGLAAGT 1238 677 YGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSG 712 1239 FGLYSWGNAGLTFDNLTVVDLKSGLEVNRIVGTNAAAETWFGLEGNDELQGF 1298 713 EGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDCGSGDDVLNGGAGNDV- 762

Qy 763YIFRKGDGNDTLYDGTGN-DKLAFADANISDIMIERTKEGIIVKRNDHS 810 bb 1359 IGGDGSDRYRYGRGDGSDVIVETASASGSVDRLSLYDIDRSEAVLRKYGQSVVIELADGE 1418 Qy 811 GSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQEL 870 bb 1419TLTLSNQLADGGIERLSFADGVVLNRGDIVKGLVNRGPVAADDGL 1463 Qy 871 KKLADENKSQKLS-ASDIASSLNKLVGSWALFGTANSVSSNAL 912 c : :	Qy 521 LL-TAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSK 566 1120 LLQTTGLMSRELTWNGATNSDKYKRGWSPMGDGVNVLRLGTYALFNDPAAQAWTDYA- 1176 Qy 567 VIQRVAETEGTDEIGLIVNAKAGNDDIFVGGKNNIDGGDGHDRVFYSKDGGFGNI 622
SULT 26 Subable phosphoesterase (EC 3.1) yvnB [imported] - Agrob Species: Agrobacterium tumefaciens Date: 22-Oct. 2001 #sequence_revision 22-Oct. 2001 #text_chan Accession: A96188 Soodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard Jodoner, B.; Hollam, C.; Allinger, M.; Doughty, D.; Scott, C ience 294, 232-2328, 2001 Title: Genome Sequence of the Plant Pathogen and Biotechnol Reference number: A97359; MUID:21608551; PMID:11743194 Accession: A96188 Status: preliminary Accession: A96188 Status: ceferences: GB:AE007870; PIDN:AAK89027.1; PID:g151588 Senetics: Agnerics: Annonsome	677 1285 713 1345 763 1405 811 1465 871
Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Match Query Matches	RESULT 27 C82521 hemolysin-type calcium binding protein XF2759 [imported] - Xylella fastidiosa (strain 9a C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Species: Xylella fastidiosa C;Species: SAug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82521 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence Nature 406, 151-157, 200 A;Aitle: The genome sequence of the plant pathogen Xylella fastidiosa. A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
Qy 170 SQSTQTIEAFSSQLAKLGSTISQAKGFSNIGN-KLONLNFSKTNLGLEIITGLLSG 224 Db 789RTLLVDNFNDGKADGWATDFGATDGNTGNFLLKGTVFSRSTTGDG 833 Qy 225 ISA-GFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALI 283 Db 834 LDAPEAALEDQSDATGNKLVYIGAQSSGWSNYVFEATL 871	A/Status: preliminary A/Status: preliminary A/Molecule type: DNA A/Residues: 1-1296 <sima 1-1206="" 1-1296="" <amania="" <sima="" a="" fesidues:="" fresidues:="" si<="" sima="" td=""></sima>
284 872 341 919 390 976	submitted to GenBank, June 2000 AjAuthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm AjAuthors: Rerreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. AjAuthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, A; Reference number: A59128 A; Reference number: A59128 A; Contents: annotation C; Genetics: A.C.R.; da Silva, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.C.R., Vergerence number: A59128
1019 AGQLRDEVWTDLDGARTACKIRSGRAIADAFEDGARVASAN	Afterne: Arife) 9 Query Match Query Match Best Local Similarity 21.6%; Pred. No. 5.18-09; Matches 215; Conservative 146; Mismatches 373; Indels 260; Gaps 46; Qy 77 LSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALA 136

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VSALGYK-TAERLGWNAIGFLADOLSAAPDMGAFDHESSSWTVIFAAADRHFITGSARSD
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                                                                                                                                                                           EAFSSQLAKLGSTISQAKGFSNIGN-KLQNL--NFSKTNLGLEIITGLLSGISAGF-ALA
                                                                                                                                                                                                                                                                                                                                             DTFYRDFTQQVALTDQAKALPFLRGSGRVRNLDEAİSLSKDLGNWVQSYSQQSTRQAQLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIYESLLLKTRMEPIYNLAEEDFVNGAWVMDW---SGVERALKQGIQRHPRDGILDAIEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DNNIGELAG----ITKLGERIKSGKAYADAFEDGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-----KNASTGKKVAAGFELSNQVIGNVTKAIS-----
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AE1905 outer membrane secretion protein alr0791 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
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C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AE1905 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana? A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                             A,Accession: AE1905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-993 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB72748.1; PID:g17130136; GSPDB:GN00179
A;Cxoss-references: strain PCC 7120
C;Genetics: A,Gene: alr0791
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Proc. Natl. Acad. Sci. U.S.A. 98, 9889-8894, 2001 A; Title: The Acad. Sci. U.S.A. 98, 9889-8984, 2001 A; Title: The Acad. Sci. U.S.A. 98, 9889-9894, 2001 A; Reference number: A95842; MUD:21396508; PMID:11481431 A; Accession: G95851 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1072 «KUR» A; Residues: 1-1072 «KUR» A; Residues: 1-1072 «KUR» A; Experimental source: strain 1021, megaplasmid pSymB A; Cross-references: GB:AL591985; PIDN:CAC48479.1; PID:g15139951; GSPDB:GN00167 A; Experimental source: strain 1021, megaplasmid pSymB B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001 A; Millo: The composite genome of the legume symbiont Sinorhizobium meliloti. A; Contents: annotation C; Genetics: A; Genetic	Qy 630TEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVG 676 Db 775 GVENILSGSGADTLVGDTA-SNWFRGALGADFIDGGAGVDTADYREKTGSVEVALS 829 Qy 677YGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLD 719 Db 830 GASDSFVFVGGVVEDTIRNIENVFGGKGNDTLTGDGLANTLAGGGADILD 889 Qy 720 GGAGDD
Query Match 6.5%; Score 301.5; DB 2; Length 1072; Best Local Similarity 20.7%; Pred. No. 1e-07; Matches 207; Conservative 140; Mismatches 346; Indels 307; Gaps 43; QY 18 TKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEDHHTETAKKSVDTVNOFL 77	AG2137 AG2137 AG2137 AG2137 AG2137 Dypothetical protein all2654 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AG2137 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S NAKazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Reference number: AG137 A;Status: preliminary A;Rosesidues: 1-1417 cKUR> A;Roses-references: G=BA000019; PIDN:BAB74353.1; PID:g17131747; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: A;Genetics: A12654
Qy 223 SGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAG 272 Db 364 GSDTADFSDKVQSVVLALNGAVDAIAAVGGTEETVRNIENITGGSGNDQFTGDAAN 421 Qy 273 LSTTGAVAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFFK 318 Db 422 TFRGGLGADVLDGGDGSDTADYGDKTVSVVTLAGANPTTAFVDGWAEDSIRNIENI 478 Qy 319 FGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGNSAAAVGSAVGTPIAL 370 Qy 319 FGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGAAAVGSAVGTPIAL 370 Db 479 IGGSGNDVLAGDGGAGTDMADYSASAKGIAVMLNGANDAKVIVGSAAEDTLR- 537	Query Match 6.2%; Score 288; DB 2; Length 1417; Best Local Similarity 21.6%; Pred. No. 7.5e-07; Accessory Accessory Accessory Accessory Bcs. Accessory Bcs. Accessory Bcs. <td< td=""></td<>

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A;Residues: 1-3083 «KUR»
A;Cross-references: GB:BA000020; PIDN:BAB78212.1; PID:g17135666; GSPDB:GN00180
A;Experimental source: strain PCC 7120
C;Genetics:
A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AH2493 A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                    376 TGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLS 435
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                                                                                                                                                                                                                                                                                                                                                                   ELNKELEAERVIAITOORWDNNIGELAGITKIGERIKSGKAYADAFEDGKKVEAGSN--- 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIF 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQ 654
                                                                                                                  LA-----KLGSTISQAKGFSNIG--NKLQ------NLNFSKTNLGLEIITGLLS 223
                                                                                                                                                                                LI-----TSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVG 335
                                        529 ILAPAL--VETSGEDAGSALNIVLVAGGEVPEEGIDVFITSDIVLTDYFG----GLEEDY 682
                                                                                        SVPYGGNLNGKPFSRGGEFLDAVYNEAGEAIGFRFRLTESFATITLNPTNREEAETDGAE 742
                                                                                                                                                                  224 GISAGPALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAG--LSTTGAVAA 281
                                                                                                                                                                                                                                 GAGNDVYIFRKGD-----GNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --STLSSFLGTALAGIELDS
                                                                                                                                                                                                                                                                                          889 YTVNPEQSSAVITIKDTPESELQVSLSTEPQVL-IETEGTVAKLNFSLSATP---PVAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQ-----IDKILQ 857
                                                                   ---DAAPDALAKASIDLI----NEIIG---NLSQSTQTI
                                                                                                                                                                                                                                                                                                                                                                                                                     493 ITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGT-
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                   KLAKGLDSVENIDRKLGKASNVL---
                                                                   LIKKG
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------DLINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSN 198

SVENIDRKLGKASNVLSTLSSFLGTALAGIE-----LDSLIKKGDAAPDALAKASI---

109

160

199 IGNKLONLNFSKTNLGLEIITGLLSGISAGFALAD-------KNASTGKKVAAGF

TLEN----GDELPSWLTFDAATRTFSGTPTNSEVDTLSIKVIATDKSQASASNVFTLTVLN 2571

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247

ELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIML-----AISPLAFMN

2572 TNDAPTLENAIADQTATEDSTFSFIIPVNTFADVDADDILA-YS---ATLEEGAALPSWL 2627

AADKFNHANAL-DEFAKQFRKFGY------DGDHLLAEYQRGVGTIE--ASL---

------TIISTALGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAM 390

2628 TFNPTNRTFAGTPINSEVGTLNIKVIATDKSSANVSDVFTL---

391 FESVANRLOGKILEWEKQNGGQNYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAIT

4 INVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGT

2232

45;

Gaps

Indels 333; Length 3083;

---LNDFIKAADELG

IARLAEEPNHTETAKKSVDT-VNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGL---D 108

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-----GTSSAD-----VLNGFGGDD---YIEGLAGNDTIDGGIGRFDRLFGGDGDDA 2831
                                                                                                         ---DIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY
                                                                                                                                                                                                         -GIIDI----SNSNGKKTQ---ALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNW
                                                                                                                                                                                                                                                                                                                                            552 QVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGQGKMN-IDGGDGHDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              611 V----FYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GKITG--
--TVAN----ADQAVAANNTFTFT
                                                               451 QQRWDNNIGELAGITKLGERIKSGK--AYADAFEDGKKVEAGSNITLDAKT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 QYRDYELRKVGYGYGYGYD------NLKSVEEVIGSQ-FNDVFK--GSKFN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | | : : | | | 2832 ITDPDGILGAHGGLGNDTINVTFAANWDNDSNPNNSPRSD-
       2669
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AH2493

AH2493

Cypechetical protein all7128 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al hypothetical protein all7128 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al Cypecies: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AH2433

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
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2876

999

763

2787

42;

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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accesson: AC1852
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000019; PIDN:BAB72322.1; PID:g17129709; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSLIKKGDAAPDALAK-ASID 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 LINEIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQN-LNFSKTNLGLEIIT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIE 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GTSAAA-----PEVSGVVALMLEANRNLGYRDIQEIL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 QGKILEWEKQNGGQNYF--------DKGY---DSRYAAYLANNLKFLSEL 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 AYSARQNDFYNVGGNYIWQINGANNFNGGGLHVSHDYGFGLVDALAAVRLAETWQKQSRF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYI-----NK----- 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 HPYRGDIV------VYLTSP-----SGVQSVLVHQPGNKEDEGDNI 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 I--DGGDGHDRVFYSKDGGF-GNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKV 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGGVGNDTLRGGRGNDTYIVNSTGDIVTENANEGIDTVQSSVTYTLGANVENLTLTGTGA 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADAN---- 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              637 INGTGNSLMNTITGNSGNNTLÄNGDÅGNDFLI--AGNGNDILMGGTGNDTMLGGGGNDTYI 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLA-QRVAAGLSTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDGKK---VEAGSNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                       354; Gaps
                                                                                                                                                                                                                                                                                                                                                                            Length 900
                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.0%; Score 280; DB 2; Length 900
Best Local Similarity 19.6%; Pred. No. 1e-06;
Matches 188; Conservative 130; Mismatches 286; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 GKASNVLSTLSSFLGTALAGIEL---
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-900 < KUR>
                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                      A; Gene: all0364
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Pypothetical protein - Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Datesion: T03518
R;Vlc6k, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A;Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003
A;Reference number: Z14955; MUID:97404404; PMID:9256491
                                                                                                                                                           GGDDTFIGGNGSDNVSGGAGNDTIFGFGGNDNLTGNDGDDILVGGSGNDRLTGGSGKDIF 2986
                                                                                         SFSSLADGIDTITDFSVADDKIRVNAAGFG-----SGLV----AGNLDASQFVLG 3032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 SAAGGDAAGDTLTSVDGVIGSAYGDSLIGFDDAVYSGSDVYTNIFYGGGGDDTIDGRGGN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reaiduea: Î-643 <VLC>
A;Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAC16171.1; PID:g3128319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGTDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKD-----GGFGNITVDG--- 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -------GGSGMDYADYSASSGAVTIDLSRW 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              764 IFRK-GDGNDTLYD-GTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWYIT 821
                                                                                                                                  SNLONYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQK 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGGQNY-FDKGYDSRYAAYLA----NNLKFLSELNKELEAERVIAITQQRWDNNIGELAG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            520 PLLTAG-----TESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAET 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGNDSI----RAGAGNDTVTGNAGNDTIDGGAGNDRLSGNDGNDLILGGAGNDTLDGGAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVGYGYGYDXLKSVEEVIGSQFND-----VFKGSK-FNDIFHSGEGDDLLDGGAGD 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 ITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTG----IIDISNSNGKKTQALHFTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGTSGFSLDPGYESASQAVTITVTDNDAYFSGSATSQLDGNQTAVVTS-----
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hypothetical protein all0364 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 280; DB 2; Length 643;
; Pred. No. 6.2e-07;
44; Mismatches 143; Indels 124;
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Best Local Similarity 26.1%;
Matches 110; Conservative 44
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A;rinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;ritle: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                         A,Status: preliminary
A,Rolecule type: DNA
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A,Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A,Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebalult, P.; Vandembol, M., Vorholer, F.J.; Weidlner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A,Reference number: A96039; MUID:21368234; PMID:11474104
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CiSpecies: Caulobacter crescentus
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CiSpecies: Caulobacter crescentus
CiSpecies: Caulobacter crescentus
CiAccession: 687572
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Dukin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
N, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87572
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                                                                                                                                    695 VDSIGDYVLENANQGTDLVQSSISYTLGNSLENLTLTGTSAINGTGNRLNNVITGNSGNN 754
                                                                                                                                                                                                                   --TSDQIDKIL 856
                                                                                                                                                                                                                                                                              755 TLNGGDGNDTLNGSAGVDTLLGGNGNDILVGGTGNDTLTGGVGRDRFTFNSRSEGIDRIT 814
                                                                                                                                                                                                                                                                                                                                       Q-DKKDGTVITSQELKKLADENKSQKLSASDIASSL---NKLVGSMALFGTANSVSSN 910
                                                                                                                                                                                                                                                                                                                                                                                                   -----VSAAGFGGGLVVGAAIASSOFLLGSAATTASH 856
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hypotherical protein SMa2111 [imported] - Sinorhizobium meliloti (strain 1021) magap. C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95405
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.;
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Surzycki, R.; Wells, D.H.; Yeh, proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
                                                                                       24;
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                                                                                                                                     454
                                                                                                                                                                                 234
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...-VDFSKESPPQLLVNLATNVASGGT---- 554
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                                                                                                                                     407 KONGGONYF---DKGYDSRYAAYLANNLKFLSELNKELEA--ERVIAI------TQQRW
                                                                                                                                                                  DNNIGELA---GITKLGERIKSGKAYADAFEDGKKVEAGSNITLDAKTGIIDISNSNGKK
                                                                                                                                                                                                                                                                                                                        512 TQALHFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVG-----YGYQST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 DINTGDNVYGFGSTQYGYQLTS-----SGMQHDIGFAIHDTGGVDTIDFSGS----
                                                                                                                                                                                                                                                                                                                                                                    -----TAGTIL--DLRAGOFSSVN----GHSNNVSIFAGHNADAADY-----
                                         Length 1112;
                                                                                       Indels
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                                         5.8%; Score 269.5; DB 2;
24.5%; Pred. No. 4.7e-06;
iive 56; Mismatches 143;
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                                                                                            Conservative
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                                                                   Similarity
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A, Genome: plasmid
                                                                      Best Local Sim:
Matches 127;
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                                              Query Match
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probable outer membrane secretion protein SMb21543 [imported] - Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: H99564

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A;Molecule type: DNA
A;Residues: 1-589 <KUR>
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hypothetical calcium binding protein [imported] - Sinorhizobium meliloti (strain 1021) m C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95995
C;Accession: E95995
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95995
A;Status: preliminary
A;Accession: E95995
A;Status: preliminary
A;Accession: E95995
A;Cross-references: GB:AL591985; PIDN:CAC49629.1; PID:g15141116; GSPDB:GN00167
A;Cross-references: GB:AL591985; PIDN:CAC49629.1; PID:g15141116; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Reference number: A95262; MUID:21396509; PMID:11481432
A; Accession: G95405
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-539 «KIR»
A; Residues: 1-539 «KIR»
A; Residues: 1-539 «KIR»
A; Residues: Cowie: Brain 1021, megaplasmid pSymA
A; Residues: Cowie: Brain 1021, megaplasmid pSymA
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebbult, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
A; Contentes: annotation
C; Genetics:
A; Gene: SMa2111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDAFLFDGMHGHAAFGDLSVKGNHLYFLDIERLSLTTGIGDDRIIATGFSFVHVHTGAGD 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TDEIGLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFY----SKDGGFGNITVDGTSATE 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIMIERTKEGIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQ 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 AGSYT---VNRKVARGD-----IYHEVVKRQETKVGKRTETIQYRDYELRKV--GYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.8%; Score 268; DB 2; Length 53:
26.4%; Pred. No. 2e-06;
tive 59; Mismatches 160; Indels
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Best Local
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hypothetical protein alr3659 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Ercain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2263
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
                                                             Comp, C.; Lelaure,
Wong, K.; Yeh, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                15;
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A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNSTGNNLLDGGEGNDEIYVYSSSGNNTLKGGVGNDILDVRFSYGKN-----ILDG 138
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Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics: A;Gene: SMb21402
A;Gene: SMb21402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 YGGVGNDRIFGGDGNDYIVGGVGDDYAE-----GGEGNDRLDGGLGNDAFMGGIGNDIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 NAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATE-----AGSYTVNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV--ARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYQSTDNLKSV---EEVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               695 QFNDVFKGSKFNDIFHSGEGDDLLD-----GGAGDDRLFGGKGNDRLSGDEGDDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 IGDDIVDGGNGNNYLDGGDGNDVLDSEGGSDEAHGGSGNDRISVGAGNDRAFGDDGDDIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        746 DGGSGDDVLNGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIM 794
                                                                                                                                                                                                                                                                                                                                                                  387;
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                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                              5.8%; Score 267.5; DB 2
30.8%; Pred. No. 1.3e-06;
iive 39; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 30.89
Matches 89; Conservative
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Db 195 NIVSGGNGN-DIFYAYGVGANTLNGGSGDDSFYISSPSADTVVHPLVTQTVDGGI 249 Qy 620 GNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELKKVGY 677	
RESULT 39 AD1841 hypothetical protein alr0276 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. PCC 7120 A;Note: Nostoc sp. ptrain PCC 7120 C;Species: Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 C;Accession: AD1841 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AD1841 A;Accession: AD1841 A;Actus: preliminary A;Molecule type: DNA A;Residues: 1-2348 ckUR> A;Accession: AD1841 A;Strain Source: strain PCC 7120 C;Genetics: A;Coss-references: GB:BA000019; PIDN:BAB77800.1; PID:g17135254; GSPDB:GN00179 A;Bxperimental source: strain PCC 7120 C;Genetics: alr0276	Oy 595 VGGCKMIDGGDGHDRVPYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVV 651 1
Query Match 5.7%; Score 266; DB 2; Length 2348; Best Local Similarity 20.4%; Pred. No. 2.1e-05; Matches 193; Conservative 121; Mismatches 332; Indels 298; Gaps 38; Qy 16 NSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAKKS 69	C;Species: Sinorhizoblum mellloti C;Dacession: S409-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: E95933 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endown A;Reference number: A95842; MUID:21396508; PMID:11481431 A;Accession: E95933 A;Status: preliminary
OY 70 VDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKSNVLSTLSS 129 1527 FDPTGQPSGSVGDKVRVTGSVSEFSTNNGVSSLTQLSSVSSILIDERMSN 1581 OY 130 FLGTALAGIELDSLIKKGDAAPDALAKASIDLINEITGNLSQSTQTIEAFSSQLAKLG 187 15	A; Rosidues: 1-387 - KUR> A; Residues: 1-387 - KUR> A; Residues: 1-387 - KUR> A; Cross-references: GB: ALS 91985; PIDN: CAC49133.1; PID: g15140618; GSPDB: GN00167 A; Experimental source: strain 1021, megaplasmid pSymb R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Ppla, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
NFSKTNLGLEIITGLLSGI TDGRLEQYTQFNDPS GPELSNQVIGNVTKAISSY GPELSNQVIGNVTKAISSY TNTLRGGDTVASITG	Science 233, 668-67, 2001 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Tetle: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: Appension A;Genetics: Appension A;Genetics: Appension
QY 279 VAALITSSIMLAISPLAFMNAADKRNHANALDEFAKGFRKF 319 DD 1729 NPRPATTPDVGGTLKVASTRVLANYFNGDGTGSGFTSPEQRGAENLTEFNRGREKITAAIL 1788 QY 320	Query Match S.7%; Score 263.5; DB 2; Length 387; Best Local Similarity 25.4%; Pred. No. 2.1e-06; Matches 99; Conservative 51; Mismatches 111; Indels 129; Gaps 15; Qy 546 GRVKNWQVTDGEASSKLDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFVGGGKNNIDGG 605

DGHDRVFY-SKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTET 664	: IQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSGEGDDLLD 719	720GGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVXIFRKGDGND 772 	TNISDIMIERTKE 800 	801 GIIVKRNDHSGSINIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKK 860 :	DGTVITSQELKKLADENKSQKLSASDIASS
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Angelos J.A., Hess J.F., George L.W.;

"Cloning and characterization of a Moraxella bovis cytotoxin gene.";

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"Cloning and characterization of a Moraxella bovis cytotoxin gene.";

"Embl. AP205359; AAK64651.1;

"InterPro; IPR001343; Hemlysn.Ca.bind.

"InterPro; IPR001343; Hemlysn.Ca.bind.

"R Pfam; PF00353; hemolysinCabind; 5.

"Pfam; PF00353; hemolysinCabind; 5.

"Pfam; PF00313; CABNDNGRPT.

"R PRINTS; PR01488; RTX7, 1.

"R PRINTS; PR01488; RTX7, 1.

"R PROSITE; PS00313; HEMOLYSIN. CALCIUM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSNINVIKSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Moraxella.
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Last annotation update)
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99.9%; Pred. No. 1.6e-199;
:ive 0; Mismatches 1;
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Q8FE01
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MEDLINE-21388402; PubMed=11497442;
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Best Local Simi
Matches 926;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                          - protein search, using sw model
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ENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLS 170
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                                                                                                                           the Leukotoxin
(Pasteurella)
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                                                                  STRAIN-PH574;
MEDLINE-21101823;
MEDLINE-21101823;
MEDLINE-21101823;
Davies R.L., Whittam T.S., Selander R.K.;
Davies R.L., Whittam T.S., Selander R.K.;
Gene in Bovine and Molecular Bvolution of the Gene in Bovine and Ovine Strains of Mannheimia (Pa haemolytica.";
D. Bacteriol. 183:1394-1404 (2001).
EMBL, AR314521; AA440305.1;
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn.Ca_bind.
InterPro; IPR003955; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF00353; RTX; 1.
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IW; 25C077858BDC76C4
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PRINTS; PRO1488; RTXCOXINA.
PROSITE; PSO0166; ENOYL COA HYDI
SEQUENCE 946 AA; 101480 WW.
Pasteurellaceae; Mannheimia.
NCBI_TaxID=85401;
                                                     FROM N.A
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                   SNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTQTIEAFS
                                                                                                                                                             SQLAKLGSTISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSGISAGFALADKNASTGK
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Q9EV24;
Q1-MAZ-201 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
10-wAR-2003 (TrEMBLrel. 23, Last annotation update)
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SGATAALVLADKNASTSRKVGAGFELANQVVGNITKAVSSYILAQRVAAGLSSTGPVAAL 300
                                                                    LEWEKQNGCONYFDKGYDSRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELA
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STRAIN=PH498, and PH344;
Davies R.L., Whittam T.S., Selander R.K.;
Sequence diversity and molecular evolution of the leukotoxin (lkta)
gene in bovine and ovine strains of Mannheimia (Pasteurella)
haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI 922
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=85401;
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Last annotation update)
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EMBL, AF314518; AAG40302.1; -.

EMBL; AF314517; AAG40301.1; -.

InterPro; IPR001753; EnCoA hydrtse.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR001395; RtxA.
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(TrEMBLrel. 16, L
(TrEMBLrel. 23, L
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01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                        SKPNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDV
                                                                                                                 YIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY---
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=85401;
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                                                                                                                                                                                                                                                                                                         SQKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI 922
                                                                                                                                                                                                                                                                                                                                 LIKHS-KNVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL 937
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PRINTS; PR01488; RIXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102150 WW; D99C36DA595B1624 CRC64;
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BMBL, AF314522; AAG40306.1; -
InterPro; IPR001753; EnCoA hydrae.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PP00353; hemolysinCabind; 5.
Pfam; PP03382; RTx7; 1.
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Best Local Similarity 49.5%; Pred. No. 2.8e-97;
Matches 471; Conservative 182; Mismatches 258;
               PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROSTITE; PRO146; BOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102135 MW; 70DB354157F5881E
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=PH496;
MEDLINE=2110182;
Packers: PubMed=11157953;
MEDLINE=2110182;
Mattam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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KVVDNYELLKHS-KWVTNSLDKLISSASAFTSSNDSRNVLVAPTSMLDQSL
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                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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49.5%; Pred. No. 2.8e-97;
ive 182; Mismatches 258;
                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammāproteobacteria;
Pasteurellaceae; Mannheimia.
NGBI_TaxID=85401;
                                                                                                      953
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PRINTS; PR01488; RTXTOXINA.
PR051TE; PS00166; ENOYL COA HYDRATASE;
SEQUENCE 953 AA, 102138 WW, C41D9EI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 183:1394-1404 (2001).
EMBL. AR344520, AAG40304.1.
InterPro: IPR001753; EnCoA hydrese.
InterPro: IPR001343; HemlyFn_Ca_bind.
                                                                                                      PRT;
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Pfam, PF00353, hemolysinCabind,
Pfam, PF02382, RTX, 1.
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  FIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITSOELKKLADENKSOKLSASDIASSLNKLVGSMALFGTANSVSSNALQPITQPTQGI 922
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                                                                                                           EIIGNLSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNLN-FSKTNLGLEIITGLL
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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01-MAR-2003
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                                                                                                                                                  TVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQ 695
                                                                                                                                                                                                      FNDVFKGSKFNDI FHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLN 755
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TPGTEHRERVQTGKYEYITKLNINRVDSWKITDGAASSTFDLTNVVQRIGIELDNAGNVT
                                                                                                            601 KTKETKIVAKLGAGDDNVFVGSGTTEIDGGEGYDRVHYSR-GNYGALTIDATKETEQGSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxi
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102236 MW; AC5874B3B75D1C98 CRC64;
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Last sequence update)
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EMBL; AF314519; AAG40303.1; -
InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn Ca bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
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J. Bacteriol. 183:1394-1404(2001).
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Bacteria, Proteobacteria, Ga
Pasteurellaceae, Mannheimia.
NCBL_TaxID=85401;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                 Davies R.L., Whittam T.S., Selander R.K., "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella) haemolytica.", J. Bacteriol. 183:1394-1404(2001).
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                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102078 WW; EF425243C8741EE4 CRC64;
                                                                                                                                                                                                 EMBL, AF314509; AAG40293.1; -...
InterPro; IPR001753; EnCoA_hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF00352; RTX1.
                                                                                   MEDLINE=21101823; PubMed=11157953;
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PRINTS; PR01488; RTXTOXINA.
                                              SEQUENCE FROM N.A.
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GGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINI
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"Sequence Diversity and Molecular Evolution of the Leukotoxin (1ktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
haemolytica ";
J. Bacteriol. 183:1394-1404(2001).
EMBL, AR314509, AR460292.1;
InterPro; 1PR001753; BnCoA hydrtse.
InterPro; 1PR001343; Hemlysn_Ca_bind.
InterPro; 1PR00353; hemolysinCabind; 5.
Pfam; PF00353; RTX; 1.
                                                                                                                                                                                                                                                 Query Match 50.3%; Score 2336.5; DB 2; Length 953; Best Local Similarity 49.6%; Pred. No. 1.9e-96; Matches 474; Conservative 181; Mismatches 256; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENVYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102132 MW; 4138ABSFAE2843B3 CRC64;
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Last sequence update)
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                                                                                                                        TISTALGAVSAGVSAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKI
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STRAIN=PH292, and PH296;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whitten T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannhelmia.
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PRINTS; PRO1488; RIXTOXINA.
PROSITE; PSO0166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102218 \( \text{IW} \), 04AB1715B819E571 CRC64;
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(lktCABD) of Mannheimia (pasteurella) Helbosida and Pasteurella trehalosi.", J. Bacterriol. 0:0-0(2001).

EMBL, AF314515; AAG40299.1; ---
EMBL, AF31411; AAL13281.1; ---
InterPro; IPR001753; BENCA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR001343; Hemlysn_Ca_bind.
                                                                                                                                                            Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
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Davies R.L., Whittam T.S., Selander R.K.;
Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102160 Ww; A189BF80754A7907 CRC64;
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InterPro; IPR001753; EnCoA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
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Pfam; PF00353; hemolysinCabind;
Pfam; PF02382; RTX; 1.
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                                         PRWY----ITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELK 871
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                                                                 GIOSILGSVLAGMDLDEAL-QNNSNQHALAXAGLELTNSLIENIANSVKTLDEFGEQISQ
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GGKGDDIFVHRQGDGNDSITESEGNDKLSFSDSNLKDLTFEKVNHHLVI-TNTKQEKVTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=PH284, PH388, and PH8;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence diversity and molecular evolution of the leukotoxin (lktA) gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica.";
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Pasteurellaceae, Mannheimia.
NCBI_TaxID=75985;
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PRINTS; PRO1488; RTXTOXINA.
PROSTIE; PSO10166; ENOYL. COB. HYDRATASE; 1.
SEQUENCE 953 AA; 101<u>9</u>97 MW; DS93D6A577C3ADE9 CRC64;
                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
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EMBL, AR1416507; AR460291.1; -.
EMBL, AR314504; AR440288.1; -.
EMBL, AR314506; AAC40290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pasteurella haemolytica.
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                                             Pasteurella haemolytica.
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                                                                                              STRAIN=PH392
                               Leukotoxin.
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                                                                    63 TETAKKSVDTVNOFLSLTQTGIAISATKLEKFLOKHSTNKLAKGLDSVENIDRKLGKASN 122
                                                                                                                                    LAKLGSTISQAKGFSNIGNKLONLN-FSKTNLGLEIITGLLSGISAGFALADKNASTGKK 241
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                                                                                                                                                                   VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD 301
                                                                                                                                                                                                     KFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVG 361
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       Length 953;
     tch 50.1%; Score 2329.5; DB 2; Length al Similarity 50.1%; Pred. No. 3.9e-96; Conservative 178; Mismatches 259; Indels
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                                                                                                                                                                                                                                                                               Davies R.L., Whittam T.S., Selander R.K., "Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
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                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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Created)
Last sequence up
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102230 WW; 28686808E
                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 183:1394-1404(2001).
BMBJ. AF34516; AAG40300.1.
InterPro: IPR001753; EnCOA hydrtse.
InterPro: IPR001343; Hemlyën_Ca_bind.
InterPro: IPR00395; KtxA.
Pfam; PF00353; hemolysinCabind; 5.
Pfam; PF02382; RTX; 1.
                                                                                                                                                                                                                                                               MEDLINE=21101823; PubMed=11157953;
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775 YDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPRWY----ITSNLQNYQSN 830
VLSGIQSILGSVLAGMDLDEAL-QNNSNQHALAKAGLELTNSLIENIANSVKTLDEFGEQ 199
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Davies R.L., Whittam T.S., Selander R.K.;
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Pasteurellaceae, Mannheimia.
NCBI_TaxID=75985;
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                                                                                                                      TVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELRKVGYGYGYQSTDNLKSVBEVIGSQ
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 953 AA; 102147 WW; 11600FDA7849ALCA CRC64;
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STRAIN=PH278;
MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of Gene in Bovine and Ovine Strains of Mannhelmia haemolytica.";
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EMBL; AF314514; AAG40298.1; -.
INTERPRO; IPR001735; ENCOA hydrtse.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR0013995; RtxA.
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Pfam; PF02382; RTX; 1.
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Bacteria, Proteobacteria, Ga
Pasteurellaceae, Mannheimia.
NCBI_TaxID=75985;
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                                                                                                                                                                                    8 KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTEŢ 65
                                                                                                                                                                                               | LDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVY1FRKGDGNDTLYDG
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                                                                                                                                                                 Gaps
"Sequence Diversity and Molecular Evolution of the Leukotoxin (1ktA) Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella) haemolyvica.";

J. Bacteriol. 183:1394-1404 (2001).

EMBL, AF314505, AAG40289.1;

InterPro; IPR001753; EnCoA_hydrtse.

InterPro; IPR001753; Hemlysn_Ca_bind.

InterPro; IPR00395; RtxA.

Pfam; PF00333; hemolysinCabind; 5.

Pfam; PF00338; RTX; 1.
                                                                                                                                                                 56;
                                                                                                                                              Length 953;
                                                                                                                                             Ouery Match 50.1%; Score 2326; DB 2; Length 9 Best Local Similarity 49.9%; Pred. No. 5.6e-96; Matches 464; Conservative 175; Mismatches 264; Indels
                                                                                              PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROSITE; PRO0166; ENOYL. COB. HYDRATASE; 1.
SEQUENCE 953 Aa; 102010 MW; DE48B28EB0EB09FB CRC64;
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Davies R.L., Whittam T.S., Selander R.K.;
Davies R.L., Whittam T.S., Selander R.K.;
Sequence diversity and molecular evolution of the leukotoxin gene in bovine and ovine strains of Mannheimia (Pasteurella) haemolytica.";
J. Bacteriol. 0:0-0(2001).
EMBL; AF314513; AAG40297.1;
EMBL; AF314513; AAG40297.1;
EMBL; AF314513; BCOADAG40297.1;
InterPro; IPR001753; EnCoA_Hydrise.
InterPro; IPR001995; RtxA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella haemolytica.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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PRINTS; PR01488; RTXTOXINA.
PROSITE; PR00166; ENOYL COA HYDRATASE; 1.
SEQUENCE 954 AA; 102410 MW; 02A60E52411711A2 CRC64;
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Last annotation update)
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llarity 49.8%; Pred. No. 1e-95;
Conservative 177; Mismatches 248;
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Query Match
Best Local Simil
Matches 458; C
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MEDLINE=21101823; PubMed=11157953;
Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxin (lktA)
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
haemolytica.";
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Bacteria; Proteobacteria; Ga
Pasteurellaceae; Mannheimia.
NCBI_TaxID=75985;
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                                                                                                                                                                                                                     LGSTISQAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA
                                                                                                                                                                                                                                   GFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRKVARGDIYHEVVKRQETK
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                                                                     AKKSVDTVNQFLSLTQTGIAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLS
                                                                                                                                                                                                                                                                                                                                                                              GTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA
                                                       KSNIQAGLNSTKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAADELGIARLAEEPNHTET
                             26;
 Length 953
                             Indels
49.6%; Score 2307; DB 2; llarity 49.3%; Pred. No. 3.9e-95; Conservative 179; Mismatches 266;
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                  Similarity
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ID Q9EV22
AC Q9EV22;
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SOOR REPORT OF THE PROPERTY OF

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KGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGN 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                EAEFAKTIONYVATR-DDKIEELIGQNGERITSKQVDELIE--KGNGKIAQSELTKVVDN 901
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     GLIVNAKAGNDDIFVGQGKMNIDGGDGHDRVFYSKDGGFGNITVDGTSATEAGSYTVNRK
                                                                                                  NVIKSNIQA---GLN-----STKSGLKNLYLAIPKD--YDPQKGGTLNDFIKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PH254, PH254, PH252, Belander R.K.;
Davies R.L., Whittam T.S., Selander R.K.;
Sequence diversity and molecular evolution of the leukotoxin (lktA)
gene in bovine and ovine strains of Mannheimia (Pasteurella)
haemolytica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 NKSOKLSASDIASSLNKLVGSMALFGTANSVSSNALOPITOPTOGILAPSV 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gammaproteobacteria; Pasteurellales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

48.9%; Score 2274; DB 2; Length 5
Best Local Similarity 48.7%; Pred. No. 1.2e-93;
Matches 463; Conservative 180; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Pasteurellaceae; Pasteurella
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                Pasteurella trehalosi.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBI_TaxID=47735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

49.2%; Score 2286; DB 2; Length 955;
Best Local Similarity 49.0%; Pred. No. 3.4e-94;
Matches 466; Conservative 177; Mismatches 264; Indels 44
                                                                                                                                                                                                                                                                                                                          Davies R.L., Whittam T.S., Selander R.K.;
"Sequence Diversity and Molecular Evolution of the Leukotoxi
Gene in Bovine and Ovine Strains of Mannheimia (Pasteurella)
                                                                                                                                                                                                                                                                                                                                                                                                haemolytica.";

Dacteriol. 183:1394-1404(2001).

EMBL; AP314526; AAG40310.1;

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR001343; Hemlysn_Ca_bind.

InterPro; IPR003895; RtxA.

Pfam; PF00353; HemlysinCabind; 5.

Pfam; PF00383; RTX; 1.

PRINTS; PR00313; CABNDNGRPT.

PRINTS; PR01488; RTXTOXINA.

PROSITE; PS00166; ENOYL COA HYDRATASE; 1.

SEQUENCE 955 AA; 102069 WW; PDCF2E99BBDC394F CRC64;
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                   MEDLINE=21101823; PubMed=11157953;
(TrEMBLrel. 16, C
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  01-MAR-2001 (
01-MAR-2001 (
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Leukotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 KGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ
                                                                                                                                                                                                                                                                   KHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLIKKGDAAPDALAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 HFTSPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVA---
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                                                                                                                                             Gaps
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                                                       PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROS175; PRO1330; HEMOLYSIN CALCIUM; 1.
SEQUENCE 956 AA; 102495 MW; 9F8EB14EC76628D5
                                                                                                                   48.0%; Score 2229.5; DB 2;
larity 47.7%; Pred. No. 1.1e-91;
Conservative 187; Mismatches 256;
       InterPro; IPR001343; Hemlyen_Ca_bind
InterPro; IPR003995; RtxA.
                                 Pfam; PF00353; hemolysinCabind; Pfam; PF02382; RTX; 1.
                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                  MLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYORGVGTIEASLTTISTA 347
                                                                                                                                                                      LGAVSAGVSAAAVGSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEK 407
SSESIAQNFSQAKTVLSGVQSILGSVLAGMDLDEAL-QNESDQLTLAKAGLELTNSLIEN 187
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                                                                       GFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSI
                        LSQSTQTIEAFSSQLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISA
                                               IANSVOTLDAFSEQISOFGSKLONVKGLGALGDKLKNIGGLDKAGLGLDVISGLLSGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RTX toxin IIA.
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579 EIGLI-----VNAK--AGNDDIFVGQGKMINDGGDGHDRVFYSKDGGFGNI---TVDG 626
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627 TSATEAGSYTVNRKVARGDIYHEVVKRQETKVGKRTETIQYRDYELR-----KVGYGYQS
                                                                                                                                                                                                                                                                                SPLLTAGTESRERLTNGKYSYINKLKFGRVKNWQVTDGEASSKLDFSKVIQRVAETEGTD
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PRINTS; PRO1488; RTXTOCNINA.
PROSTITE; PRO0330; HEMOLYSIN CALCIUM; 1.
SEQUENCE 987 AA; 105662 WW; CC34CD62BF9B745D CRC64;
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Last annotation update)
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larity 47.5%; Pred. No. 2.6e-88;
Conservative 167; Mismatches 266;
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Vet. Microbiol. 87.159-174 (2002).
EMBL, AF381184; AAM45566.1;
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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STRAIN-CUGG 19799;
MEDLINE-22031201; Pubmed-12034544;
Berthoud H., Frey J., Kuhnert P.;
"Characterization of Agx and its of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00353; hemolysinCabind; 1.
Pfam; PF02382; RTX; 1.
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Bacteria, Proteobacteria, Gammap
Pasteurellaceae, Actinobacillus
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Best Local Simi
Matches 463;
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Pasteurellaceae, Actinobacillus.
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                               GTVITSQELKKLADENKSQKLSASDIASSLNKLVGSMALFGTANSVSSN
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"Characterization of Agx and its operon: the hem of Actinobacillus equull.";

Vet. Microbiol. 87:159-174 (2002).

EMBL, AF381185; AAM45569.1;

InterPro; IPR001343; Henlysn_Ca_bind.

InterPro; IRR03995; RtxA.

Pfam; PF00335; hemolysincabind; 3.

Pfam; PF02382; RTX; 1.
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                      279 VAALITSSIMLAISPLAFMNAADKFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIE
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                                                                            TGLLSGISAGFALADKNASTGKKVAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGA
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A Heyberger-Meyer B., Frey J., Nicolet J., Kuhnert P.;
Heyberger-Meyer B., Frey J., Nicolet J., Kuhnert P.;
Indentification and characterization of a new RTX toxin operon (pax in Pasteurella aerogenes.";
Lubmitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U66588; ARF1370.1;
R InterPro; IPR001343; Hemlyen Ca_bind.
R InterPro; IPR001343; Hemlyen Ca_bind.
R Ffam; PF00353; Hemlyen Cabind; 6.
R Pfam; PF00353; Hemlyen Cabind; 6.
R PRINTS; PR00319; CABNDNGRPT.
R PRINTS; PR00310; HEMULYSIN CALCIUM; 1.
R PROSITE; PS00330; HEMULYSIN CALCIUM; 1.
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                                                                             Gammaproteobacteria;
23, Last annotation
                                                  rasteurella aerogenes.
Bacteria; Proteobacteria; Gam
Pasteurellaceae; Pasteurella.
NCBI_TaxID=749;
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912 HNNRVLIKDWF-----KEGNKYNHKIEQIVDKNGRKLTAENLGTYFKNAPKADNLLN 964
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                                                                                         ITSSIMLAISPLAFMNAADKFNHANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLT
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MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Ilouu S.-R., Boutin A., Hackett J., Stroud
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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Enterobacteriaceae, Bscherichia.
NCBI_TaxID=217992;
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SEQUENCE FROM N.A.
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GEGNDKLFGGNGNNYLSGGDGDDELQVLGNGFNVLRGGKGNDKLYGGAGSDFLDGGEGDD
                                                                                                                                                                                                                                                                                                                   753 VLNGGAGNDVYIFRKGDGNDTLYD---GTGNDKLAFADANISDIMIERTKEGIIVKRNDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RTX-Coxin IIIA.
Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae)
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
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Pfam; PF00313; hemolysincabind; 6.
PRINTS; PR00131; CABNDNGRP.
PRINTS; PR01488; RTATOXINA.
PROSITE; PR00330; HEMOLYSIN CALCIUM; 1.
SEQUENCE 1052 AA; 112862 WW; CA0E160F02101F42 CRC64;
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Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S.,
"Cloning and Sequencing of Apx IIIA from Actinobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pleuropneumoniae.";
Submitted (MAR.2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR3631363; AAK56053.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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Conservative 167;
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                                                     tch al Similarity 41.8%; Score 1848.5; DB 16; Length 1024; al Similarity 41.8%; Pred. No. 1.4e-74; 428; Conservative 153; Mismatches 310; Indels 132;
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"Extensive mosaic structure revealed by the complete
     of uropathogenic Bscherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
EMBL; AE016766; AAN82018.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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Best Local Similarity 42.1%; Pred. No. 1.9e-74;
Matches 424; Conservative 153; Mismatches 303; Indels 128;
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                                                                                       QLAKLGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGK
                                                                                                              FEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGK
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
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                                                                                                              GKYEYITELLVKGVDKWTVKGVQDKGSVYDYSNLIQHASVGNNQYREIRIESHLGDGDDK 622
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EMBL, AJ494981; CAD42039.1; -. SEQUENCE 1024 AA; 110365 MW; 3F3C284A45FEFEB3 CRC64;
                                                                                                                                                                                     860 HIIDDDGGKDDKLSLADIDFRDVAFKREGNDLIMYKAEGNVLSIGHKNGITFRNWF----
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Enterobacteriaceae; Escherichia.
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                                     -GGKGNDRLSGDEGDDLLDGGSGDDVLNGGAGNDVYIFRKGDG
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                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid EHEC-hemolysin plasmid.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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40.4%; Pred. No. 9.7e-71;
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InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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STRAIN=enterohemorrhagic EC920006;
MEDLINE=98261495; PubMed=9596716;
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                                                                                                                                                                                                                                                                                                                                                    63 TETAKKSVDTVNQFLSLTQTGIAISATKLEKFLQ--KHSTNKLAKGLDSVENIDRKLGKA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    647 YHEVVKRQETKVGKRTETIQYRDYEL--RKVGYGYGYGTDNLKSVEEVIGSQFNDVFKGSK
                                                                                                                                                                                                                                                                            Gaps
                                                                Kolodrubetz J., Dailey T., Kraig E.; "Nucleotide sequence of the leukotoxin gene from actino-bacillus Actinomycetemcomitans: Homology to the A-hemolysin/leukotoxin gene
                                                                                                                                                                                                                                                   Ouery Match 39.1%; Score 1816; DB 2; Length 1055; Best Local Similarity 40.2%; Pred. No. 4e-73; Matches 413; Conservative 185; Mismatches 299; Indels 130;
                                                                                                                                                                                      PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PRO1488; RTXTOXINA.
PROSUTE; PS00330; HEMCLYSIN CALCIUM; 1.
SEQUENCE 1055 AA, 113853 WW, 5331C396FA76669E CRC64;
                                                                                                             Infect. immun. 58:920-929(1991).
EMBL; X16829; CAA34731.1; -.
InterPro; IPRO01343; Hemlyen_Ca_bind.
InterPro; IPRO03995; RtxA.
Pfam; PF00353; hemolysinCabind; 6.
Pfam; PP02382; RTX; 1.
     Pasteurellaceae; Actinobacillus
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                                         SEQUENCE FROM N.A.
                NCBI_TaxID=714;
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                                                                                              RYAAYLANNLKFLSELNKELEAERVIAITOORWDNNIGELAGITKLGERIKSGKAYADAF 481
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                                SYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGLIVNAKAGNDDI-F 594
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                                                                                                                                              KFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVG 361
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                                                                              VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD
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Enterobacteriaceae; Escherichia.
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Q9LC58;
Q1-OCT-2000 (TrEMBLrel. 15, L5
Q1-MAR-2003 (TrEMBLrel. 23, L6
Hemolysin A.
EREC-HIYA.
Escherichia coli.
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VANDINKIISSVSGFDSGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDS 421
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Taneike I., Wakisaka-Saito N., Harada Y., Zhang H.-M., Yamamoto T.;
"The enterohemorrhagic Escherichia coli (EHEC)-hemolysin genes of a
Shiga toxin 1 (Srx1)- and Srx2-producing, serotype 0128 Escherichia
coli strain with a greatest hemolytic activity.";
Acta Med. Biol. (Niigata) 0:0-0(2000).
EMBL, AB032930; BAA93708.1; -.
InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR00355; RtxA.
Pfam; PF00353; hemolysinCabind; 6.
                                                                                                                                                                                                                              Length 998;
                                                                                                                                                                                                  CD7A88E9BD862DB6 CRC64;
                                                                                                                                                                                                                                           Best Local Similarity 40.4%; Pred. No. 1.2e-70;
Matches 396; Conservative 174; Mismatches 305;
                                                                                                                                                                                                                              37.9%; Score 1760; DB 2; 40.4%; Pred. No. 1.2e-70;
                                                                                                                                                                                    CALCIUM;
                                                                                                                                                                                                  998 AA; 107196 MW;
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PRINTS; PRO1488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN G.
PROGENCE 998 AA; 107196 M
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                                                                                                                                                                               SRYAAYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADA 480
                                                                                                                                                                                                                          788 QAHGAYNILSGGTGDDKLYGGGGIDLLDGGEGNDYLNGGFGNDIYVYRQNYGHHTIADEG
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                                                                                                                                                                                                                                                                                                                                      481 FEDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGK
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                               361 GSAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYD
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Plasmid p0157.
Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete nucleotide sequences of 93-kb and 3.3-kb plasmids of enterohemorrhagic Escherichia coll 0157:H7 derived from Sakai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=98290540; PubMed=9628576;
Makino K., Ishii K., Yasunaga T., Hattori M., Yokoyama K.,
Yatsudo H.C., Kubota Y., Yamaichi Y., Iida T., Yamamoto K.,
Han C., Ohteubo A., Kasamatsu M., Hayashi T., Kuhara S.,
Shinagawa H.,
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NCBI_TaxID=83334;
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SEQUENCE OF 241-998 FROM N.A.
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with diarrhea and hemolytic-
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                                                                               ---NDHSGSINIPRWYITSNLQN
                                                                                                                                                                                                                                  827 YQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 KSNIQAGLNSTKSGLKNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEPNHTETAK
                                                                                                                                                       848 GKGDRLHLSDISFDDIAFKRVGNDLIMNKAINGVLSFNESNDVNG-ITFKNWFAKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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Last annotation update)
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llarity 40.1%; Pred. No. 1.8e-70;
Conservative 176; Mismatches 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97034624; PubMed=880480; Schmidt H., Karch H.; Schmidt H., Karch H.; Schmidt H., Karch H.; Enterchemolytic phenotypes and genoty[es pof Esherichia coli 0111 strain from patients wit uremic syndrome."; J. Clin. Microbiol. 34:2364-2367(1996). EMEL; X94129; CAA63849:1; -. InterPro; IPR001343; Hemlysn.Ca_bind. InterPro; IPR001343; Hemlysn.Ca_bind. Pfam; PF00353; hemolysinCabind; 6. Pfam; PF00353; hemolysinCabind; 6. Pfam; PF00353; hemolysinCabind; 6. Pfam; PR01382; RTX; J. PRINTS; PR01488; RTXTOXIA. PRINTS; PR01488; RTXTOXIA. SEQUENCE 998 AA; 107255 MW; DA3EF078C7E41
                                                                                   TGNDKLAFADANISDIMIERTKEGIIVKR-----
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01-FEB-1997 (TrEMBLrel. 0:
01-MAR-2003 (TrEMBLrel. 2:
EHEC-hemolysin.
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SEQUENCE FROM N.A. Shin S.J., Park J.Y., Choi I.S., Shin N.R., Yoo H.S., "Cloning and Sequencing of Apx IA from Actinobacillus
                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PRINTS; PR01488; RTXTOXINA.
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Matches 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFV 595
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                                                                                                                                                                                                                                                                                                                                                                                             LSSFLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQTIEAFSSQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAKLGSTISQAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 VAAGFELSNQVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAAD 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFNHANALDEFAKQFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVG 361
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                                                                                                                                                                                                                                                                                                                                              19 KSAFNTASSSVRSAGKKLILLIPDNYEAQ-GVGINELVKAADELGIEIHRTERDDTAIAN 76
                                                                                                      "The complete DNA sequence and analysis of the large virulence plasmid of Escherichia coli 0157:H7.";

Of Escherichia coli 0157:H7.";

EMBL; AB011549; BAA31774.1;

EMBL; AP074613; AAC10116.1;

INCEPPO; IPR001343; Hemlysn_Ca_bind.
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                          102;
                                                                                                                                                                                                                                                                                  37.6%; Score 1748; DB 2; Length 9:
llarity 40.0%; Pred. No. 4.1e-70;
Conservative 177; Mismatches 308; Indels
              Hall R.H., Xu J., Walderhaug M.O.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            998 AA; 107047 MW; BB3C0D36FCBB9EBD CRC64;
                                                                      MEDLINE=98391744; PubMed=9722640;
Burland V., Shao Y., Perna N.T., Plunkett G.,
Blattner F.R.;
                                                                                                                                                                                                   Pfam; PF00353; hemolysinCabind; 6.
Pfam; PF02382; RTX; 1.
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PRINTS; PR01488; RTXTOXINA.
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Matches 391; Conserve
                                                SEQUENCE FROM N.A.
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175 234 789 AHGAYNILSGGTGDDKLYGGGGIDLLDGGEGNDYLNGGFGNDIYVYGQNYGHHTIADEGG 848 GNDYIEGNYGNDRLYGDDGDDYISGGQGDDQLFGGSGNDKLSGGDGNNYLTGGSGNDELQ 788 ------DLLDGGSGDDVLNGGAGNDVYIFRKGDGNDTLYD-GT 778 GNDKLAFADANISDIMIERTKEGIIVKR------NDHSGSINIPRWYITSNLONY 827 QSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDI 887 9 80 61 NHTETAKKSVDTVNQFLSLTQTGIAISATKLEKFLOKHSTNKLAKGL-DSVENIDRKLGK 176 IEAFSSQLAKLGSTISQAKGFSNIGNKLONL-NFSKTNLGLEIITGLLSGISAGFALADK 8 KSNIQAGLNSTKSGL-----KNLYLAIPKDYDPQKGGTLNDFIKAADELGIARLAEEP ASNVLSTLSSPLGTALAGIELDSLIKK----GDAAPDALAKASIDLINEIIGNLSQSTQT RTX toxin IA. Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae) Actinobacillus pleuropneumoniae) Pasteeria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Actinobacillus. 37.4%; Score 1736; DB 2; Length 1022; llarity 39.4%; Pred. No. 1.4e-69; Conservative 178; Mismatches 317; Indels 120 Submitted (MMR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF363361; AAK50051.1; -. InterPro; IPR001343; Hemlysn_Ca_bind. InterPro; IPR003995; RtxA. 1022 AA; 110439 MW; A68E486D335467E3 CRC64;

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GNDYIEGNYGNDRLYGDDGDDYISGGQGDDQLFGGSGNDXLSGGDGNNYLTGGSGNDELQ 788
                                                                 Schmidt H., Kernbach C., Karch H.,
"Analysis of the EHEC hly operon and its location in the physical map
of the large plasmid of enterohemorrhagic Esherichia coli 0157:H7.";
Microbiology 142:907-914 (1996).
EMBL, X86087; CAA60042.1,
InterPro: IPR001343; Hemlysn_Ca_bind.
InterPro: IPR001343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 6.
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39.9%; Pred. No. 1.7e-69;
tive 174; Mismatches 312; Indels 102;
                                                                                                                                                                                                                                                                                                998 AA; 107032 MW; 4D8BE108C309BF7E CRC64;
[2]
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STRAUNEEL 933;
MEDLINE=97090409; PubMed=8936317;
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Enterobacteriaceae; Escherichia.
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MEDLINE=95172699; PubMed=7868227;
Schmidt H., Beutin L., Karch H.;
"Molecular analysis of the plasmid-encoded hemolysin of coli 0157:H7 strain Ed1933.";
Infect. Immun. 63:1055-1061(1995).
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                                                                                                                                                              RYAAYLANNIKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAF 481
                                                                                                                                                                                              SYINKLKFGRVKNWQVTDGEASSK--LDFSKVIQRVAETEGTDEIGLIVNAKAGNDDIFV 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QETKVGKRTETIQYRDYELRKVGYGYQSTDNLKSVEEVIGSQFNDVFKGSKFNDIFHSG- 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNDYIEGNYGNDRLYGDDGDDYISGGGGDDQLFGGSGNDKLSGGDGNNYLTGGSGNDELQ
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KFERAKQLESYSERFKKLNYEGDALLAGFHKETGAIDAGLTTINTVLSSVSAGVSAASSA
                                                      SAVGTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDS
                                                                                                                                                                                                                                                                            EDGKKVEAG----SNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKY
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=519;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
01-MAR-2003 (ETEMBLrel. 24, Last annotation update)
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                                                            789 AHGAYNILSGGTGDDKLYGGGGIDLLDGGEGNDYLNGGFGNDIYVYGQNYGHTIADEGG 848
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                                                                                                                                                                                                                                                                                  LAKLGSTISQAKGFSNIGNKLONL-NPSKTNLGLEIITGLLSGISAGFALADKNASTCKK 241
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                                                                                                                                                                                                                                                  QSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDI 887
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                                                                                                                                                                       GNDKLAFADANISDIMIERTKEGIIVKR------NDHSGSINIPRWYITSNLQNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Matches 389; Conservative 174; Mismatches 313; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 998;
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Pfam; PF00382; RTX; 1.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01489; RTXTOXINA.
SEQUENCE 998 AA; 107058 MW; 0D3BE108C309B8B3 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNVTKAISSYVL----AQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNHANAL 309
                                                                                                                                                                                                                                                                                                                                                 | | | | : : : | | : | : | | : | GSRSFSLGEVSDMAAVEAAELEMTRQVLHAGARQDDAEPGVSGASAHW
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                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                          tch al Similarity 27.2%; Score 799; DB 2; Length 1706; al Similarity 27.2%; Pred. No. 2.3e-27; 247; Conservative 143; Mismatches 347; Indels 170;
                                                                                                                                                                                                                                                                                                             GLDSVENIDRKLGKASNVLSTLSSFLGTALAGIELDSLI-----KKGDAAP-
                                                                                                                                        71750E2D0BBF3B64 CRC64;
                       PRINTS; PRO0313; CABNDNGRPT.
PRINTS; PR01488; RTXTOXINA.
PROSITE; PS00330; HEMOLYSIN CALCIUM; 3.
                                                                                                                                        177038 MW;
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                                                                                                                                        1706 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     758 AGNDVYIFRKGDGNDTLYDGTGNDKLAFADANISDIMIERTKEGIIVKRNDHSGSINIPR
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MEDINB-2056517;
PubMed=10910347;
MEDINB-20565717;
MEDINB-20565717;
Peinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
Barros M.H., Bonacocrsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 VDNYQLLKYS-RDASNSLDKLISSASAFTSSND-SRNVL---ASPT-SMLDPSL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             874 ADENKSOKLSASDIASSLNKLVGSMALFGTANSVSSNALOPITOPTOGILAPSV
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Xanthomonadaceae; Xylella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 233
                                                                                                                                                                                                                                                                                                                                                STRAIN=TIO SEROTYPE AND T3 SEROTYPE;
Lainson A.F., Altchison K.D., Donachie W.;
Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; Z22884; CAA80501.1; --
EMBL; Z22884; CAA80498.1; --
HSSP; Q30323; IRAR.
InterPro; IFR01343; Hemlysn Ca bind.
PF00353; hemolysinCabind; 4.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hemolysin-type calcium binding protein.
                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.4%; Score 482; DB 2;
Best Local Similarity 41.5%; Pred. No. 2.1e-14;
Matches 97; Conservative 53; Mismatches 70.
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233
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                                                          Created)
                        Q51865; Q51867;
01-NOV-1996 (TrEMBLrel. 01, C.
01-NOV-1996 (TrEMBLrel. 01, L.
01-MAR-2003 (TrEMBLrel. 23, L.
Leukotoxin A (Fragment).
Pasteurella haemolytica.
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   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       982 GSNRLEGGAGNDVLKVSÝWSADNVLIG----GTGDDTLYGS---AFADTYLFNQGD--GH 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 AKGFSNIGNKLQNLNFSKTNLGLEIITG-----LLSGISAGFALADKNASTGKKVAAGFE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 LSNQVIGNVTKAI--SSYVLAORVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFNH 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 ANALDEFAKQFRKFG-----YDGDHLLAEYQRGVGTI------EAS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 LTTISTALGAVSAGVSAAAVG-SAVGTPIALLVAGVTG---LISG----ILEASKQAMFE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393 SVANRLOG-----KILEWEKON---GGONYFDKGYDSRYAAYLANNLKFLSELNKELE 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 AERVIAITQQRWDNNIGELAGITKL--GERIKSGKAYADAFEDGKKVEAGSNITLDAKTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   793 MYLALP---PRQLSATFDAFAEAYAKLKESIYIRLVLEPRLTDYLSG-----LRLTD 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TG--IAISATKLEKFLQKHSTNKLAKGLDSVENIDRKLGKASNVLSTLSSFLGTALAGIE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      842 NNGVMAWDASGLEAKLDQTWQHNKAQALQDVMDLYR---YGSNAV-----AASGWK 889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 LYLAIPKDYDPQKGGTLNDFIKAADELG---IARLAEEPNHTETAKKSVDTVNQFLSLTQ 81
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Purlan L.R., Gardean J.S., Franca S.C., Franco M.C., Frohme M., Purlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Lemos B.C., Lemos M.V., Lenes M.R., Leite L.C.C., Lemos E.G.M., Lemos M.N., Madeira J.R., Matchado J.R., Marques M.N., Madeira A.M.B., Madeira H.M.F., Marsino C.L., Marques M.V., Martins E.A.L., Martins E.A.L., Matchira H.R., Matsukuma A.Y., Monco D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S., Mani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., Madeira G.G., Rouries L.R., Oliveira M.A., Persira G., Persira H.A. Jr., Pesquero J.B., Quaggio R.B., Persira G.G., Persira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., As Silva M.A., da Silva M.A., da Silva M.A., da Silva M.A., da Silva M.A., Tazi S.M., Tsuhako M.H., Vallada H., Van Sluys M.A., Verjovski.Almeida S., Vettore A.L., Mature 406.;151-154(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SNRLEGGAGDDVLKVSYWSADNVLSGG----TGDDTLYGSAFADTYLF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 415; DB 16; Length 1636; larity 22.4%; Pred. No. 3.2e-10; Conservative 150; Mismatches 323; Indels 308
                                                                                                                                                                                                                                                                                                                                                                                                                       1636 AA; 173012 MW; 76A6E54271859CB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00353; hemolyginCabind; 18.
PRINTS; PR00313; CABNDNGRPT.
PRINTS; PR01488; RTXTCXINA.
PROSITE; PS00330; HEMOLYSIN_CALCIUM; 4.
                                                                                                                                                                                                                                                                                                                      InterPro; IPR001343; Hemlysn_Ca_bind.
InterPro; IPR003995; RtxA.
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EMBL; AE003938; AAF83821.1; -.
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                                                                                                                                        ---- DIFV-GQGKMNIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KVGKRTETIQYRDYELRKVGYGYQSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             841 GKDGSYITSDQIDKILQDKKDGTVITSQELKKLADENKSQKLSASDI 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                        561 KLDFSKVIQRVAETEGT-----DEIGLIVNAKAGND---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hemolysin-type calcium binding protein.
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
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NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 697 NDVFKGSKFNDIFHSGEGDDLLDGGAGDDRLFGGKGND--RLSGDEGDDLLDGGSGDDVL 754
                                                                                                                                                                                                                      86 ISATKLEKFLOKHS-----TNKLAKGLDSVENID--RKLGKASNVLSTLSSFLGTALA 136
                                                                                                                                                                                                                                    DIQLGLEHFYRDYSGAHDKVTVSDAARALPAISGSGAVRDLREAASLSPALLAAVQALTP 401
                                                                                                                                                                           QKGGTLNDFIKAADELGIARLAEEPNHTETAKKSVDTVNQFL----SLTQTG----IA 85
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                                                                                                                                                                                                                                                                                                           171 -----QSTQTIEAF-SSQLAKLGSTISQAKGFSNIGNKLQNLNFSKTNLGLEIITGLLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 KAGND-----DIFV-GQGKMNIDGGDGHDRV------FYSKD----GGFGN
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Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meddanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
EMBL; AE003910; AAF83478.1; -.
EMBL; AE003910; AAF83478.1; -.
PinterPro.; IRROL1343; Hemlysn.Ca bind.
Pfam; PF00313; hemolysinCabind; 15.
PRINTS; PR00313; CABNDNGRPT.
                                                                                                                                Query Match 8.8%; Score 411; DB 16; Length 1208; Best Local Similarity 22.0%; Pred. No. 3.1e-10; Matches 227; Conservative 169; Mismatches 344; Indels 294;
                                                                                                            1208 AA; 128403 MW; DF151ACD7741872B CRC64;
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                                                                                                 Complete proteome.
SEQUENCE 1208 A
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RAM Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alves L.M.C., Arraya J.E., Baia G.S., Baptista C.S., Rayerenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Rayerenga R., Alves L.M.C., Araya J.E., Baca G.S., Baptista C.S., Rayerenga R.H., Bonacocoxis B.D., Bordin S., Bove J.M., Bilones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., R.A., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., R.A. Fraga J.S., Ferreira V.E.A., Ferreira V.E., Ferro J.A., R.A. Fraga J.S., Ferreira W.C.A., Ferro J.A., R.A. Fraga J.S., Ferreira W.C.A., Ferro J.A., R.A. Fraga J.S., Ferreira W.C.A., Ferro J.A., R.A. Fraga J.S., Ferreira W.C.A., Ferro J.A., R.A. Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajima J.P., R.A. Krieger J.E., Kuramae E.B., Landais M.R., Leite L.C.C., R.A. Mardiac M.M., Madeira A.M.B.N., Madeira B.M.F., Martins E.M.F., Martins C.L., Martins E.M.F., Martins C.L., Martins E.A.L., Martins E.M.F., Martins C.L., R.A. Mani A. Jr., Nobrega F.G., Miyaki C.Y., Monteiro-Vitorello C.B., R. Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteira M.R., Pagus A.J., M.A., A.J., Pesquero J.B., R.A. de Sliva A.G., Pergira H.A. Jr., Pesquero J.B., R.A. de Sliva A.G., Pergira H.A. Jr., Pesquero J.B., R.A. de Sliva A.G., Pergira H.A., Jr., Sawasaki H.E., da Silva R.A., Truffi D., Tsai S.M., Tsuhako M.H., R.A. Zago M.A., Zatz M., Meidanis J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Truffi D., Tsai S.M., Tsuhako M.H., R.A. Zago M.A., Zatz M., Meidanis J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Truffi D., Tsai S.M., Tsuhako M.H., R. Nadianis J., Salveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C., Silveiria J.C
                                                                                                                                                                                                                                                                                          814 NIPRWYITSNLQNYQSNKTDHKIEQLIGKDGSYITSDQIDKILQDKKDGTVITSQELKKL
                                                                                                                              NGGAGNDVYIFRKGDGNDTLYDGTGNDKLAFADA-NISDIMIERTKEGIIVKRNDHSGSI
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Xanthomonadaceae; Xylella.
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Last sequence update)
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InterPro; IPR001343; Hemlysn Ca bind.
Pfam; PF00353; hemolysinCabind; 31.
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PROSITE; PS00330; HEMOLYSIN_CALCIUM;
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 25.4;
Matches 135; Conservative
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Complete proteome.
SEQUENCE 2064 AA
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446 VIAITQQRWDNNIGELAGITKLGERIKSGKAYADAF----EDGKK--VEAGSNITLDAKT 499
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01-NOV-1996 (TEXBELREI. 01, Last sequence update)
01-NOV-1996 (TEXBELREI. 23, Last annotation update)
Leukorcoxin A (Fragment).
Pasteurella haemolytica.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
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STRAIN=T4 SEROTYPE;
Lainson A.F., Altchison K.D., Donachie W.;
Submitted (UN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; Z22885; CAA80499.1; -.
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US-08-630-916A-38
US-09-071-035-436
US-09-732-210-765
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US-09-252-911A-27285
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US-09-107-512A-6895
US-09-107-512A-6895
US-09-26-965-125
US-09-252-991A-23093
US-09-134-001C-4521
US-09-252-991A-2673
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APPLICANT: Xu, Jian Guo

TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.

TITLE OF INVENTION: A New and Distinctive DNA Sequence of E.

Patent No. 5756293

TITLE OF INVENTION: Coli O157:H7 and its Use for the Rapid, Sensitive and
TITLE OF INVENTION: E. coli
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29

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APPLICANT: HALL, Robert H.
APPLICANT: XU, Jian Guo
ITILE OF INVENTION: COLI OL57:H7 AND ITS FOR THE RAPID, SENSITIVE AND
ITILE OF INVENTION: COLI OL57:H7 AND ITS USE FOR THE RAPID, SENSITIVE AND
ITILE OF INVENTION: SPECIFIC DETECTION OF OL57:H7 AND OTHER ENTEROHEMORRHAGIC
                                  Gaps
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: FU-LUDS/NB-LUDS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,813
FILING DATE: 11.5EP-1995
CLASSIFICATION NUMBER: US/08/526,818
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/258,188
FILING APPLICATION NUMBER: US 08/258,188
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 15.280-206-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.5%; Score 14; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 0;
   Pred. No. 0.00022;
                               Mismatches
                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08526813; Patent No. 5756293; GENERAL INFORMATION:
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100.08;
                                                                                                                               379 ISGILEASKQAMFE 392
                                                                                          379 ISGILEASKQAMFE 392
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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US-08-526-813-2
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Sequence 2, Application US/08258188

Patent No. 5475098

GENERAL INFORMATION:
APPLICANT: XU, Jian Guo
TITLE OF INVENTION:
APPLICANT: XU, Jian Guo
TITLE OF INVENTION: A NEW AND DISTINCTIVE DNA SEQUENCE OF E.
TITLE OF INVENTION: SPECIFIC DEFECTION OF O157:H7 AND OTHER ENTEROHEMORRHAGIC
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPENDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                   24803, A
18268, A
29676, A
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6481, Ap
4325, Ap
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27528, A
9, Appli
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18559, A
2, Appli
2, Appli
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ZIP: 94105-1493

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NaTA:
APPLICATION NUMBER: US/08/258,188
FILING DATE: 14-7UN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REGISTRATION NUMBER: 15280206, DHHSE135940
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 101601
                                                                                                                                                                                                                                                                                                                         US-09-252-91A-24803
US-09-252-991A-18268
US-09-252-991A-29676
US-09-615-192A-397
US-09-328-352-6481
US-09-328-352-6481
US-09-328-352-6481
US-09-292-8888-23
US-09-252-991A-27528
                                                                                   US-09-252-991A-21150
US-09-560-507-19
US-09-136-801-19
US-09-136-801-19
US-09-134-001C-5508
US-09-252-991A-18559
US-07-989-485-2
PCT-US93-11298-2
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         -09-198-452A-857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

    758 amino acida
amino acid

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RESULT 1

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Query Match

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Best Local Similarity 100.0
Matches 14; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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US-09-062-126-10
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Patent No. 6019384

GENERAL INFORMATION

APPLICANT: Macinnes, Janet

APPLICANT: Maliard, Bonnie

APPLICANT: Maliard, Bonnie

APPLICANT: Rosendal, Soren

TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR

TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bereskin & Parr

STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.5%; Score 14; DB 5; Length 758; Best Local Similarity 100.0%; Pred. No. 0.00022; Matches 14; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: E. coli
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk

COMPUTER IN FOCOMPATION:

COMPUTER: IN PC COMPATION:

COMPUTER: IN PC COMPATION:

COMPUTER: IN PC COMPATION:

COMPUTER: IN PC COMPATION:

COMPUTER: IN PC COMPATION:

COMPUTER: IN PC COMPATION:

APPLICATION NUMBER: PCT/US95/08554

FILING DATE: 14-UNN-1994

CLASSIFICATION:

NAME: GATCATLON:

ATTORNEY/AGENT INFORMATION:

NAME: GATCATLON:

NAME: GATCATLON:

NAME: GATCATLON:

NAME: GATCATLON:

TELEPHONEY/AGENT NUMBER: 15280206, DHHSE135940

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

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TELEPHONE: (415) 543-603

TELEPHONE: (415) 543-603

TELEPHONE: (415) 543-603

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-560

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TELEPHONE: (415) 543-560

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TELEPHONE: (415) 543-560

TELEPHONE: (415) 543-503

TELEPHONE: (415) 543-560
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APPLICATION NUMBER: US/08/772,270A FILING DATE: December 23, 1996 CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 ISGILEASKQAMFE 165
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-772-270A-11
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; Batent No. 6500435
; GENERAL INFORMATION:
; APPLICANT: Ramp. Elbarte Margriet
; APPLICANT: Smits, Marinus Addianus
; TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
; FILE REPRENCE: 470-980537
; CURRENT APPLICATION NUMBER: US/09/062,126
; CURRENT APPLICATION NUMBER: 08/418,706
; PRIOR APPLICATION NUMBER: 08/418,609
; PRIOR FILING DATE: 1993-10-15
; PRIOR FILING DATE: 1993-10-15
; PRIOR FILING DATE: 1993-10-15
; PRIOR FILING DATE: 1993-10-15
; PRIOR FILING DATE: 1993-10-15
; PRIOR FOLICATION NUMBER: 07/722,971
; PRIOR PRING DATE: 1993-10-15
; SOFTWARE: FastEEQ for Windows Version 3.0
; SOFTWARE: FastEEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 14; DB 3; Length 1049;
100.0%; Pred. No. 0.00029;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: Recombinant Vaccine For Procine
TITLE OF INVENTION: Pleuropneumoniae
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Alan S. Korman
STREET: 1600 Empire Tower
CITY: Buffalo
CITY: Buffalo
STATE: Wew York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                MOLECULE TYPE: protein

CRIGINAL SOURCE:
CREANISM: Actinobacillus pleuropneumoniae
US-08-772-270A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Actinobacillus pleuropneumonia
US-09-062-126-10
REFERENCE/DOCKET NUMBER: 6580
TELECOMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
SEGUENCE CHARACTERISTICS:
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275 KVAAGPELSNQVIG 288
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GENERAL INFORMATION:

APPLICANT: Kamp, Elbarte Margriet

APPLICANT: Shites, Marinus Adrianus

APPLICANT: Shites, Marinus Adrianus

APPLICANT: Shites, Marinus Adrianus

TITLE OF INVENTION: Recombinant Vaccine For Prevention

TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections

FILE REPRESENCE: 470-980537

CURRENT APPLICATION NUMBER: 08/09/062,126

CURRENT FILING DATE: 1998-04-17

PRIOR APPLICATION NUMBER: 08/138,609

PRIOR APPLICATION NUMBER: 08/138,609

PRIOR APPLICATION NUMBER: 08/138,609

PRIOR APPLICATION NUMBER: 07/122,971

PRIOR APPLICATION NUMBER: 07/722,971

PRIOR APPLICATION NUMBER: 07/722,971

PRIOR ELLING DATE: 1993-10-15

SEQ ID NOS: 15

SEQ ID NO 8

LENGTH: 956
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APPLICANT: Kamp, Elbarte Margriet
APPLICANT: Smits, Marinus Adrianus
ITILE OF INVENTION: Recombinant Vaccine For Prevention
TITLE OF INVENTION: And/Or Treatment Of Pleuropneumonia Infections
FILE REFERENCE: 470-980537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 0.17;
tive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.2%; Score 11; DB 3; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Actinobacillus pleuropneumonia
US-09-062-126-8
          ATTORNEY AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 6580-81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 956 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09062126 Patent No. 6500435
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369 ALLVAGVIGLI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 ALLVAGVTGLI 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 ALLVAGVTGLI 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 ALLVAGVTGLI 402
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-772-270A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-062-126-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
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Sequence 8, Application US/08772270A

Sequence 8, Application US/08772270A

Patent No. 6019984

GENERAL INFORMATION:
APPLICANT: Maclatti, Paul
APPLICANT: Ricciatti, Paul
APPLICANT: Rosendal, Soren

TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
INUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COMPTRY: Canada
ZIP: MSH 3Y2

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIBLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Detember 23, 1996

FILING DATE: December 23, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5%; Score 14; DB 5; Length 1244; 100.0%; Pred. No. 0.00034; tive 0; Mismatches 0; Indels
                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/10500
FILING DATE:

CLASSIFICATION DATA:

FILING DATE:

ATPORNEY/AGENT INFORMATION:

NAME: ATTORNEY/AGENT INFORMATION:

NAME: ATTORNEY/AGENT INFORMATION:

TELEBRACATION NUMBER: 33,932

REGISTRATION NUMBER: 33,932

REGISTRATION NUMBER: 31,932

REGISTRATION NUMBER: 31,9603/00001

TELECOMMUNICATION INFORMATION:

TELEBRACATION NUMBER: 19603/00001

TELEBRAX: 716-853-8104

TELEBRAX: 716-853-8109

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Actinobacillus pleuropneumoniae STRAIN: Sercypes 2, 3, 4, 6 and 8 INDIVIDUAL ISOLATE: Swine CELL TYPE: Gram negative bacterium
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1244 amino acids
TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KVAAGFELSNOVIG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 KVAAGFELSNOVIG 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 14; Conserva
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Gaps

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NSG-252-149B-26
Sequence 26, Application US/09252149B
Sequence 26, Application US/09252149B
Sequence 26, Application US/09252149B
Sequence 26, Application US/09252149B
SERENT INFORMATION:
APPLICANT: Barker, Christopher A.
APPLICANT: Moreav, Mohamad
TITLE OF INVENTION: VERTEBRATE SUBJECTS
TITLE REPERBRECE: 9001-0042
CURRENT APPLICATION NUMBER: US/09/252,149B
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: 60/075,213
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                                                                                                                                                                                                                     Sequence 45, Application US/08387942C
; Sequence 45, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
    APPLICANT: EXTESVAG, HELGA
    APPLICANT: SKJAK-BRAEK, GUDMUND
    APPLICANT: LARSEN, BJORN
    APPLICANT: LARSEN, BJORN
    TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
    TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
    NUMBER OF SEQUENCES: 52
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: BIRCH, STEMART, KOLASCH & BIRCH, LLP
    STREET: P.O.BOX 747
    CONTRICTOR TO SEQUENCES
    STREET: P.O.BOX 747
    CONTRICTOR TO SEQUENCES
    STREET: P.O.BOX 747
    CONTRICTOR TO SEQUENCES
    STREET: P.O.BOX 747
    CONTRICTOR TO SEQUENCES
    STREET: P.O.BOX 747
    CONTRICTOR TO SEQUENCES
    STREET: P.O.BOX 747
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100.0%; Pred. No. 0.27;
ive 0; Mismatches 0; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,942C FILING DATE: 09-MAY-1995 CLASSIFICATION: 435
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     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURENY JK, GERALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 180:
TELECHONE: 703-205-8000
TELEPHONE: 703-205-8050
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 10; Conservative
                                                     266 AQRVAAGLSTT 276
                                                                                                      289 AORVAAGLSTT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22042
COMPUTER READABLE FORM:
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                                                                                                                                                                                                       US-08-387-942C-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-387-942C-45
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APPLICANT: Miciatti, baul
APPLICANT: Miciatti, baul
APPLICANT: Mallard, Bonnie
APPLICANT: Rosendal, Soren
TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                 1.2%; Score 11; DB 4; Length 1013;
100.0%; Pred. No. 0.18;
ive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,270A
FILING DATE: December 23, 1996
CLASSIFICATION: 424
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Best Local Similarity 100.0%; Pred. No. 0.18;
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                  CURRENT FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 08/488,706
PRIOR FILING DATE: 1995-06-09
PRIOR FILING DATE: 1995-06-09
PRIOR FILING DATE: 1993-10-15
PRIOR FILING DATE: 1993-10-15
PRIOR FILING DATE: 1991-06-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
CURRENT APPLICATION NUMBER: US/09/062,126
CURRENT FILING DATE: 1998-04-17
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Actinobacillus pleuropneumonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gravelle Micheline
REGISTRATION NUMBER: 40,261
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08772270A
Patent No. 6019984
GENERAL INFORMATION:
APPLICANT: MacInnes, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMPION LALLON ASSESSED TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 AQRVAAGLSTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 AQRVAAGLSTT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 11; Conserva
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                                                                                                                                                                                                                                                                                     LENGTH: 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: ....

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-MG-1996
CLASSIFTCATION: 424
ATTORNEY AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INDER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TRIEPHONE: (415)327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-178-10

US-08-178-10

US-08-178-10

Sequence 10 Application US/08878748

Sequence 10 Application US/08878748

Sequence 10 Application US/08878748

GENERAL INFORMATION:
APPLICANT: REDMOND, MARK J.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                   US-08-694-865-10
Sequence 10, Application US/08694865
Sequence 10, Application US/08694865
Sequence 10, Application US/08694865
Sequence 10, Application US/08694865
Sequence 10, Application US/08694865
SEQUENCE 10, ADDREW A.
SEPLICANT: POTTER, ANDREW A.
STATE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
SADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 LAQRVAAGLS 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: leukotoxin polypeptide carrie
1971ER INFORMATION: Figures 15A-15D
US-09-252-1498-26
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                                                                                                                                                                                                                                                                                                    Query Match
1.1%; Score 10; DB 4; Length 490;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IS FORM:

COMPUTER: IS FORM:

SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,156
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: REDMOND, WARK J.
APPLICANT: HOUGHES, HUW P.A.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
COMESSEE: ADDRESS:
ADDRESSEE: AS BRYANT STREET
CITY: PALO ALITO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-387-156-10
; Sequence 10, Application US/08387156
; Patent No. 5723129
                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-387-156-10
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100.0%; Pred. No. 0.86;
live 0; Mismatches 0; Indels
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1.1%; Score 10; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 34301
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09383912

Patent No. 6521746

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
                                                NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REPRENCE/DOCKET NUMBER: 9001-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415)327-3400
                                                                                                                                                                                                                                      LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 10; Conservative
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100.0%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 19.00/108/07/108
CLASSIFICATION DATA:
APPLICATION NUMBER: 080/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 080/960,932
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: 080/960,932
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 080/779,171
FILING DATE: 10-CCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10. Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STRET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
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CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 544 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||||||
256 LAQRVAAGLS 265
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 LAQRVAAGLS 274
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US-09-124-491-10
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Gaps
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Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
FILING DATE:
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-383-912-16

Sequence 16, Application US/09383912

Sequence 16, Application US/09383912

Sequence 16, Application US/09383912

SEREMAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
ITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
                                                                                                                                                                                       PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/79,171
ATTORNEY AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REFERENCE DOCKET NUMBER: 98.548
REFERENCE DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415)327-3400
TELEFAX: (415)327-3340
TELEFAX: CONCRETE OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US OF US 
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REGISTRATION NUNBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 699 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-124-491-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 LAORVAAGLS 274
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                  US-UW-694-865-16

Sequence 16, Application US/08694865

Patent No. 5837268

GENERAL INPORMATION:
APPLICANT: POTTER. ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS NUMBES DE SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: REED & ROBINS LLP STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECPMUNICATION INFORMATION:
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Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: FORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPASIBLE
COMPUTER: IBM PC COMPASIBLE
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 699 amino acids
amino acid
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256 LAQRVAAGLS 265
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Best Local Similarity
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US-09-124-491-16
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Sequence 2, Application US/07908253

Patent No. 5534256

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HARLAND, RICHARD J.
TITLE OF INVENTION: PROPEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ENHANCED INMUNOGENICITY USING LEUKOTOXIN TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: RED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 926;
1.4;
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                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PALO ALTO
SOFTWARE: PATENTIN POLOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/908,253
FILLING DATE: 19920702
CLASSIFICATION: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9000-0026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEPAX: (415) 327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                   DB 4; Length 699;
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Sequence B, Application US/08619812

Sequence B, Application US/08619812

Sequence B, Application US/08619812

SEMERAL INFORMATION:

APPLICANT: POTTER, ANDREW A.

APPLICANT: THEISEN, MICHARD.

TITLE OF INVENTION: VACCINES FOR HAEMOPHILUS SOMNUS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: REED & ROBINS

STREET: 635 BRYANT STREET

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94301
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Pasable Form:
COMPUTER: Pasable Form:
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100.0%; Pred. No. 1...
... 0; Mismatches
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TELEFAX: (415)32/-32.
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 699 antho acids TYPE: amino acid
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amino acid
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                               Query Match 1.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                   TOPOLOGY: 'linear'; MOLECULE TYPE: protein US-09-383-912-16
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Gaps
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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REPRENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 RESULT 25
US-08 694-865-6
US-08 694-865-6

j Sequence 6, Application US/08694865

j Patent No. 5837268

j GENERAL INFORMATION:
APPLICANT: POTTER. ANDREW A.
APPLICANT: MANNS, JOHN G.

TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 26
US-08-878-748-6
US-08-878-748-6
Sequence 6, Application US/08878748
Settlent No. 5969126
GENERAL INFORMATION. ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRAH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.1%; Score 10; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415)327-3400
TELEFAK: (415)327-3231
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 926 amino acids
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              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-387-156-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 LAQRVAAGLS 274
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amino acid
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100.0%; Pred. No. 1.4;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITATE: 013 BEKANI SIREE!
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
ATPONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/779,171
ATPONEY/AGENT INFORMATION:
AND ATTER 16-OCT-1991
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08387156

Patent No. 5723129

GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: HUGHES, HUW P.A.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                              CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-0CT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REGISTRATION NUMBER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 327-3331

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 926 amino acide

TYPE: amino acide

TYPE: amino acide

TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: ROBINS, ROBERTA I.

REGISTRATION UNDRER: 33,208

REFERENCE/DOCKET NUMBER: 9001-0016.21

TELECOMMUNICATION INFORMATION:
                     APPLICATION NUMBER: US/08/455,970A FILING DATE: 31-MAY-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 617-8999
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10; Conservative
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-455-970A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 LAQRVAAGLS 265
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                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
US-08-387-156-6
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926 amino acids

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FILING DATE:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/694,865

FILING DATE: 09-AUG-1996

APPLICATION NUMBER: US 08/387,156

FILING DATE: 10-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/779,171

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: MCCRACKEN, THOMAS P.

REGISTRATION NUMBER: 38,548

REFERENCE/DOCKET NUMBER: 9001-0016.22

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: (415)327-3340

TELEFRAX: (415)327-3340

SEQUENCE CHARACTERISTICS:

LENGTH: 926 amino acide

TYPE: amino acide

TYPE: amino acide

TYPE: amino acide

TYPE: amino acide
     CLASSIFICATION: 424
ATTORNEY/AGENT INRORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFRENCE/DOCKET NUMBER: 9001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             : 926 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 LAQRVAAGLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 LAORVAAGLS 265
                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                               US-08-535-837-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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Sequence 2, Application US/08535837

Sequence 2, Application US/08535837

Sequence 2, Application US/08535837

Sequence 2, Application US/08535837

Sequence 3, Application:

APPLICANT: HARLAND, RICHARD, STRCHARD, STATES OF INVENTION: HARMOPHILUS SOWNUS OUTER MEMBRANE

TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS

TITLE OF INVENTION: PROTEIN EXTRACT ENRICHED WITH IRON-REGULATED PROTEINS

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROBERTA L. ROBINS

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                    COMPTRY: UNA.-

ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIPICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
RIOR APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-CT-1991
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-CT-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
''ne: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,837
FILING DATE: 27-SEP-1995
                                                       STREET: 635 BRYANT STREET
STATE: PALO ALIFO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 LAQRVAAGLS 265
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Query Match
1.1%; Score 10; DB 2; Length 926;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                               RESULT 28
US-09-124-491-6
; Sequence 6, Application US/09124491
; Patent No. 6022960
; GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNE, JOHN G.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
ADDRESSEE: ABDRESSEE;
ADDRESSEE: ABMILTON AVENUE, SUITE 200
CITY:
CITY:
CITY:
PALO ALTO
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Gaps

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1.1%; Score 10; DB 1; Length 934;
100.0%; Pred. No. 1.4;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                        DB 6; Length 926;
1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                               Fequence 80, Application US/08215805A

Fatent No. 555908

GENERAL INFORMATION:
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTEURELLA
TITLE OF INVENTION: SUIS
NUMBER OF SEQUENCES: 84

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051

CITY: Rochester
STREET: New York

COUNTRY: USA
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRI: USA

ZIP: 14603

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LIBRARY: P. suis DNA in Bacteriophage lambda-dash; CLONE: (Lambda)yfc33-37
US-08-215-805A-80
                                                                                                                                                                                                        1.1%; Score 10; DB 100.0%; Pred. No. 1.4 tive 0; Mismatches
FILING DATE: 09-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,850
FILING DATE: 05-APR-1990
APPLICATION NUMBER: 335,018
FILING DATE: 07-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pasteurella suis
STRAIN: 5943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 934 amino acids TYPE: amino acid
                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: 5943
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
US-08-215-805A-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                            SEQ ID NO:3:
                                                                                                                                                                 5476657-3
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                                                                DB 3; Length 926;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA LEUKOTOXIN; COMPOSITIONS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09383912
Patent No. 6521746
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GRAH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/694,865
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMSS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 3901-0016.22
TELECOMMUNICATION INFORMATION:
                                                              1.1%; Score 10; DB 100.0%; Pred. No. 1.4 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/15,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 amino acids
TYPE: amino acid
                                                              Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-912-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||||||||||
256 LAQRVAAGLS 265
    MOLECULE TYPE: protein
                                                                                                                                                  265 LAQRVAAGLS 274
                                                                                                                                                                                      256 LAQRVAAGLS 265
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;Patent No. 5476657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94301
        ; MOLECULE 1ry
US-09-124-491-6
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1.1%; Score 10; DB 1; Length 943;
100.0%; Pred. No. 1.4;
ive 0; Mismatches 0; Indels
COMPUTER READABLE FORM:

MEDITUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 31-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: US 07/960,932

FILING DATE: 14-OCT-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA L.

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELECOMMUNICATION NUMBER: 33.208

REFERENCE/DOCKET NUMBER: 9001-0016.10

TELEPHONE: (415) 327-331

INFORMATION FOR SED ID NO: 10: SEQUENCE CHARACTERISTICS:

LENGTH: 943 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: AMINO acids

TYPE: AMINO acids

TYPE: AMINO acids

TYPE: AMINO acids

TYPE: AMINO acids
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APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.10
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.1
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 LAQRVAAGLS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 LAQRVAAGLS 274
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                                                         Sequence 12, Application US/08455970A

Patent No. 5708155

GENERAL INCRAMINATION

APPLICANT: POTTER, ANDREW A.

APPLICANT: HUGHES, HUW P.A.

ITLE OF INVENTION: CHIMERAS

NUMBER OF SEQUENCES: 15

COURRESPONDENCE ADDRESS:

ADDRESSEE: REED & ROBINS

STREET: 285 HAWILTON AVENUE, SUITE 200

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTY: PALO ALTO

STATE: CALIFORNIA

COUNTY: PALO ALTO

STATE: CALIFORNIA

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: PADO ALTO

SOFTWARE: Patentin Release #1.0, Version #1.25

COMPUTER: 19401

COMPUTER: 139 ANDRESS: APPLICATION DATA:

APPLICATION NUMBER: US/08/455,970A

FILING DATE: 14-0C1-1992

CLASSIFICATION NAMBER: US 07/960,932

FILING DATE: 14-0C1-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROBINS, ROBERTA 10.

RESTERENCE/DOCKET NUMBER: 901-0016.10

TELECOMMUNICATION NUMBER: 901-0016.10

TELECOMMUNICATION NUMBER: 9120A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08455970A
Sequence 10, Application US/08455970A
Patent No. 5708155
GENERAL INFORMATION:
APPLICANT: HUGHER, HUW P.A.
APPLICANT: HUGHER, HUW P.A.
TITLE OF INVENTION: CHIMERAS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STREET: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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1.1%; Score 10; DB 1; Length 936;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 327-3400
TELEPAX: (415) 327-3231
INFORMATION FOR SEO ID NO: 12:
SEQUENCE CHARACTERISTICS:
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amino acid
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US-08-455-970A-10
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                                                                                                                                                                                                             1.1%; Score 10; DB 1; Length 951; 100.0%; Pred. No. 1.4; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDWOND, WARK J.
APPLICANT: HUGHES, HW P.A.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STRATE: CALIFORNIA
STRITE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
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APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016,21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08387156
Patent No. 5723129
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 951 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                             , MOLECULE TYPE: protein US-08-455-970A-14
                                                                                                                                                                                                                                                                                                       265 LAQRVAAGLS 274
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Best Local Similarity
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                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                Query Match
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MEDIUM TYPE: Floppdish

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/694,865

FLING DATE: 09-AUG-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MCCRACKEN, THOMAS P.

REPERENCE/POCKET NUMBER: 9001-0016.22

TELECOMMUNICATION: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONDUTER TO STATES OF AMERICA
ZIP: 94301
CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1%; Score 10; DB 2;
100.0%; Pred. No. 1.5;
iive 0; Mismatches
                                                                                   APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
ADDRESSEE: REED & ROBINS LLP
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRRH-LEUKOTOXIN CHIMERAS
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STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08878748;
Patent No. 5969126;
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUW P. A.
TITLE OF INVENTION: GRRH-LEUKOTOXI
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBBINS
ADDRESSEE: REED & ROBBINS
ADDRESSEE: REED & ROBBINS
                 Sequence 8, Application US/08694865; Patent No. 5837268; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 100.
Matches 10; Conservative
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TOPOLOGY: linear
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COUNTRY:
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US-08-694-865-8
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100.0%; Pred. No. 1.5;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 Query Match 1.1%; Score 10; DB 3; Length 977; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
APLICATION NUMBER: US 08/694,865
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.3
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 38,548
REFREENCE/DOCKET NUMBER: 9001-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)327-3400
FELEFAX: (415)327-3400
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
SEGUECULE TYPE: protein
US-09-124-491-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/09383912; Patent No. 6521746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415)327-3400
TELEFAX: (415)327-3231
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: protein
US-09-383-912-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 LAQRVAAGLS 274
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COMPUTER READABLE FORM:
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US-09-383-912-8
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100.0%; Pred. No. 1.5;
tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-124-491-8
Sequence 8, Application US/09124491
Patent No. 6022960
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
TITLE OF INVENTION: GARH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: ADDRESSEE:
ADDRESSEE: ADDRESSEE: ADMILTON AVENUE, SUITE 200
                          FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PIOR APPLICATION DATA: 408 1387,156
FILING DATE: 10-FEB-1995
FILING DATE: 10-FEB-1995
FILING DATE: 11-FEB-1995
FILING DATE: 14-OCT-1992
FILING DATE: 14-OCT-1992
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELEPHONE: (415) 617-899
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TTORNEY AGENT INFORMATION:
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 977 amino acids
TTORNEY AGENT INFORMATION:
TELEPHONE: (415) 327-3231
TELEPHONE: (415) 327-3231
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CLASSIFICATION NUMBER: US/05/124,431
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
PILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
PRIOR APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION NUMBER: US 07/779,171
APPLICATION NUMBER: US 07/779,171
ATTORNEY/AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
          APPLICATION NUMBER: US/08/878,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.1
Best Local Similarity 100.
Matches 10; Conservative
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CITY: PALO ALTO
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GENERAL INFORMATION:
APPLICANT: GEORGE, LISLE W
APPLICANT: ANGELOS, JOHN A
APPLICANT: HESS, JOHN F
TITLE OF INVENTION: MORAZELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
TITLE OF INVENTION: AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
TITLE OF INVENTION: BOVIS INFECTIONS
FILE REPREMENCE: 481.06
CURRENT APPLICATION NUMBER: US/09/884,696
CURRENT FILING DATE: 2001-06-19
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Sequence 2, Application US/09884696

Publication No. US2030035809A1

GENERAL INFORMATION:

APPLICANT: GEORGE, LISLE W

APPLICANT: HESS, JOHN A

TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES

TITLE OF INVENTION: AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA

TITLE NEFERENCE: 481.06

CURRENT APPLICATION UNMBER: US/09/884,696

CURRENT FILING DATE: 2001-06-19

NUMBER OF SEQ ID NOS: 41

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Sequence 212, App Sequence 512, App Sequence 511, App Sequence 511, App Sequence 213, App Sequence 213, App Sequence 216, App Sequence 216, App Sequence 216, App Sequence 216, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 31, App Sequence 211, App Sequence 211, App Sequence 211, App Sequence 211, App Sequence 212, App Sequence 212, App Sequence 212, App Sequence 221, App Sequence 221, App Sequence 221, App Sequence 221, App Sequence 221, App Sequence 30397, App Sequence 30397, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Sequence 321, App Se
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Matches 926; Conservative
    ; TYPE: PRT
; ORGANISM: Moraxella bovis
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 695
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Best Local Similarity 100.
Matches 11, Conservative
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Matches 10; Conservative
                                                                           369 ALLVAGVIGLI 379
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US-09-305-924-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-305-924-13
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US-09-884-696-3
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Publication No. US20030035809A1
GENERAL INFORMATION:
APPLICANT: GEORGE, LISLE W
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN A
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APPLICANT: HESS, JOHN A
APPLICANT: GEORGE SOURCE SOURCE
AND APPLICANT: TILLE OF INVENTION: MORER: US/09/884,696
CURRENT PILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN Ver. 2.1
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1.5%; Score 14; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14; DB 11; I
Pred. No. 0.00032;
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NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
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                                                                                                                                                TYPE: PRT
ORGANISM: Moraxella bovis
US-09-884-696-13
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ORGANISM: Moraxella bovis
US-09-884-696-6
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US-09-884-696-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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JAPPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIKAWA, JUN
APPLICANT: HATTORI KABANITA
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: JP 2001-204089
FRIOR FILING DATE: 2001-06-02
RIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12788
LENGTH: 307
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 299-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12748
LENGTH: 259
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US-10-156-761-14641
; Sequence 14641, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INPORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, UUN
; APPLICANT: HORIKAWA, HIROSHI
NappLICANT: MANAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                               Score 9; 1
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12748
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) WITH IMPROVED PROPERTIES
FILE REPERENCE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILLING DATE: 2002-02-21
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  APPLICANT: ANGELOS, JOHN A
APPLICANT: HESS, JOHN A
APPLICANT: HESS, JOHN P
TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
TITLE OF INVENTION: AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
TITLE OF INVENTION: BOVIS INFECTIONS
FILE REPRESENCE: 491.06
CURRENT APPLICATION NUMBER: US/09/884,696
CURRENT FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 41
SCOTWARE: PALENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 953
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; LOCATION: (1)..(1017)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-20166
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Pred. No.
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
US-09-884-696-3
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.1%; 'Best Local Similarity 100.0%; Matches 10; Conservative 0
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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20166
LENGTH: 1017
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                           Indels
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION WUMBER: US/10/369,493 PRIOR FILING DATE: 2003-02-28 PRIOR FILING DATE: 2002-02-10 PRIOR FILING DATE: 2002-02-10 PRIOR FILING DATE: 47374 ERQ ID NOS: 47374 LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)..(489)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-16555
                                                                                                                                                                                                                                                                                                                             0.9%; Score 8; DB 1
100.0%; Pred. No. 1.1
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16555, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    , ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-18633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
GRANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                        Query Match 0.99
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-369-493-17426
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Publication No. US20030233675A1

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

APPLICANT: Gldman, Barry S.

PITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052) B.

CURRENT APPLICATION NUMBER: US/10/369, 493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 17978
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Sequence 18633, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Chen, Xianfeng

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(424)
; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-17978
TITLE OF INVENTION: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPRENEE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14641
LENGTH: 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       0.9%; Score 8; 1
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149 AAPDALAK 156
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298 AAAVGSAV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AAAVGSAV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 AAPDALAK 254
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US-10-369-493-17978
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Sequence 10178, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (5206.2)
CURRENT FILING DATE: 2003-02-28
FRIOR PAPLICANION NUMBER: US 60/360,039
FRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10178
LENGTH 4327
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Sequence 80, Application US/2030228607A1

GENERAL INFORMATION: US20030228607A1

GENERAL INFORMATION: Therapeutics, Inc.

APPLICANT: X-CEPTO: Therapeutics, Inc.

TITLE OF INVENTION: Screening method and modulators having an improved therapeutic

TITLE OF INVENTION: Drofile

FILE REFERENCE: 8012-002-08

CURRENT APPLICATION NUMBER: US/10/414,692

CURRENT FILING DATE: 2003-04-14

PRIOR APPLICATION NUMBER: 60/372,650

PRIOR FILING DATE: 2002-04-15

NUMBER OF SEQ ID NOS: 86

SSOTIMARE: PatentIn version 3.2

LENGTH: 20
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100.0%; Pred. No. 8.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                             Length 773;
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                                                                                                                                                           Query Match 0.9%; Score 8; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: magnetite-containing magnetic coccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(4327)
COTHER INFORMATION: unsure at all Xaa locations US-10-369-493-10178
                                                  TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.9
Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Artificial
FEATURE:
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                                                                                                           US-10-369-493-1471
; SEQ ID NO 1471
; LENGTH: 773
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        0.9%; Score 8; DB 12; Length 505; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11340, Application US/10156761
SERRAL INFORMATION:
APPLICANT: ISTERNAMATION:
APPLICANT: ISTERNAMA, JUN
APPLICANT: ISTERNAMA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIKAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-39
FRIOR APPLICATION NUMBER: UP 2001-272697
FRIOR APPLICATION NUMBER: UP 2001-272697
FRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11340
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17426
LENGTH: 505
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Publication No. US20030233675A1
GENERAL INFORMATION:
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US-10-156-761-11340
                                                                                                                                                                      TYPE: PRT ORGANISM: Bacillus halodurans
                                                                                                                                                                                                                                                                           Query Match 0.9
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-156-761-11340
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                                                                                                                                                                                                                                                                                                           APPLICANT: JOHN N. SIMONS
APPLICANT: JOHN N. SIMONS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DEARY
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUBRHOFF
APPLICANT: ANTHONY COTT MUBRHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: LABORATURIS AND METHODS FOR THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                   0.8%; Score 7; DB 12; Length 20;
100.0%; Pred. No. 50;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: BY PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PSTENTING RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
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No. 1
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ATTORNEY/AGENT INFORMATION:
NAME: POREMBERI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.8%; Score 7;
100.0%; Pred. N
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; Sequence 3945, Application US/10264049
; Publication No. US20040005579A1
                                                                                                                                                                                                                                                       Sequence 519, Application US/08424550B Publication No. US20020119447A1 GENERAL INFORMATION:
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100.0%; Pre-
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INFORMATION FOR SEQ ID NO: 519:
SEQUENCE CHARACTERISTICS:
                Query Match
Best Local Similarity 100..
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Best Local Similarity 100.
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                                                                                                                  744 LLDGGSG 750
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US-10-414-692-80
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GURBEAL INVENTION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR PILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

SOFTWARE: PATENTION NUMBER: US 60/209,467

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: PATENTIN VET: 3.1

SEQ ID NO 3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185, 050
FILING DATE: 28-Jun-2002
CLASSIFICATION NUMBER: US/08/826,516
APPLICATION DATA:
NAME: MISROCK, S. LESLIE
NAME: MISROTINFORMATION:
NAME: MISROTINFORMATION:
NAME: MISROTINFORMATION:
TELECOMMINICATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
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Ouest Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0;
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ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 52 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-10-264-049-3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 ELDSLIK 145
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Gaps

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Indels

DB 9; Length 89; . 2.1e+02;

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US-09-864-408A-5506

Sequence 5506, Application US/09864408A

Sequence 5506, Application US/09864408A

Sequence 5506, Application No. US2040009474A1

GENERAL INFORMATION:

APPLICANT: Brimkets, Richard A.

TITLE OF INVENTION: No. US20040009474A1e1 Human Polynucleotides and Polypeptides Encory:
FILE REFERENCE: 21402-012

CURRENT APPLICATION NUMBER: US/09/864,408A

CURRENT PILING DATE: 2001-05-24

FRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 9068

SEQ ID NO 5506

LENGTH: 90
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0.8%; Score 7; DB 12; L.
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: 36 Human Secreted Proteins TITLE OF INVENTION: 36 Human Secreted Proteins FILE REFERENCE: P2022P1
CURRENT APPLICATION NUMBER: US/09/938,671
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/348,457
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: 1998-01-07
PRIOR APPLICATION NUMBER: 00/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ. ID NOS: 196
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (89)
; OTHER INFORMATION: Xaa equals stop translation
US-09-938-671-83
                    ; LOCATION: (89)
; OTHER INFORMATION: Xaa equals stop translation
US-09-739-907-83
                                                                                                                                                                 0; Mismatches
                                                                                                                    Score 7; |
Pred. No.
                                                                                                                                                                                                                                                                                                                                                            US-09-938-671-83
; Sequence 83, Application US/09938671
; Publication No. US20040002066A1
; GENERAL INFORMATION:
                                                                                                                 Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
LOCATION: (89)
NAME/KEY: SITE
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                                               0.8%; Score 7; DB 15; Length 52; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0; Indels
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DS-09-739-90/-83

Patent No. US20010012889A1

GRNERAL INFORMATION:
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GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRIE REFERENCE: PZ022P1
FILE REFERENCE: PZ022P1
FURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 1990-01-07
PRIOR APPLICATION NUMBER: 60/070,567
PRIOR FILING DATE: 1998-01-07
PRIOR PILING DATE: 1998-01-07
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PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
SROFTWARE: PALCATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 196
SEQ ID NO 83
LIENGTH: 89
                                                                                                                                                                                                                                                                                                                                                  GAPERAL INC. USCUSLOUSESPAIL
APPLICANT: Murphy, Christopher J.
APPLICANT: McAulty, Jonathan F.
APPLICANT: McAulty, Jonathan F.
APPLICANT: Reid, Ted W.
TILE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: 05/21,632
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTIN UNSER: 60/290,932
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/09917340
; Patent No. US20020090369A1
                           Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                               243 AAGFELS 249
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US-09-917-340-9
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  US-10-185-050-78
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Gaps ö

Length 89; Indels

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APPLICANT: Nacett, Rachel E.
APPLICANT: Macett, Rachel E.
APPLICANT: Macett, Rachel J.
APPLICANT: Macett, Rachel J.
APPLICANT: Welcer, Rachel J.
APPLICANT: Welcer, Rachel J.
APPLICANT: Welch, Rolling Proces, J.
APPLICANT: Welch, Nadine S.
APPLICANT: Welch, Nadine S.
APPLICANT: Welch, Nadine S.
APPLICANT: Melch, Nadine S.
APPLICANT: Coland, Pret J.
APPLICANT: Coland, Pret J.
APPLICANT: Coland, Pret J.
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; OTHER INFORMATION: Amino acid consensus sequence
US-10-410-764-20
                                                                                                                                                            RESULT 29
US-10-410-764-20
; Sequence 20, Application US/10410764
; Publication No. US20040005664A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11108, Application US/09815242
Patent No. US2002006156941
CENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
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761 DVYIFRK 767
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US-09-924-358-20
Squence 20, Application US/09924358
Squence 20, Application US/09924358
Patent No. US20020107376A1
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: MacBerb, Kyle
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 26199, 33530, 33949, 47148, 50226, AND
TITLE OF INVENTION: 88764, MAND TRANSFERASE FAMILY MEMBERS AND USES THEREFOR
TITLE OF INVENTION: NOVEL HUMAN TRANSFERASE FAMILY MEMBERS AND
TITLE OF INVENTION NUMBER: US/09/924,358
CURRENT APPLICATION NUMBER: US 60/229,300
PRIOR PAPLICATION NUMBER: US 60/229,300
PRIOR PLING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 52
SQ ID NO 20
LENGTH: 102
LENGTH: 102
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                                  FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1)
CTHER INFORMATION: Wherein Xaa may be any naturally occuring amino acid
US-09-864-408A-5506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFRENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 3335
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0.8%; Score 7; DB 12; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                             Query Match 0.8%; Score 7; DB 12; Length 90; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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US-09-924-358-20
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ORGANISM: Homo sapiens
      ORGANISM: Homo sapiens
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APPLICANT: Zyskind, Judith
APPLICANT: Dohlsen, Kari L.
APPLICANT: Trandick, John
APPLICANT: Trandick, John
APPLICANT: Trandick, John
APPLICANT: Trandick, John
APPLICANT: Trandick, John
APPLICANT: Trandick, John
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: ESCHERICHIA COLI
FILE OF INVENTION: ESCHERICHIA COLI
FILE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA ADDICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2000-01-23
FRIOR PRILATION NUMBER: 09/492,709
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 465
SCOTTARER: Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fastere Fas
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APPLICANT: Oblean, Kari L.
APPLICANT: Wall, Dadith W.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tranimoto, Robert T.
APPLICANT: Wall Percent J.
APPLICANT: Wall Percent J.
APPLICANT: Wall Percent J.
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APPLICANT: Wall J.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: 1000-03-21
CURRENT FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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Pred. No. 2.4
0; Mismatches
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                                 Sequence 321, Application US/09912020 Patent No. US20020045592A1
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Best Local Similarity 100.
Matches 7; Conservative
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US-09-912-020-321
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                                                                                            APPLICANT: Xamamucu, Nobell 1.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DECKARYOLES
FILER REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
FRIOR APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/203,23
PRIOR APPLICATION NUMBER: 60/203,727
PRIOR APPLICATION NUMBER: 60/203,727
PRIOR APPLICATION NUMBER: 60/203,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2000-11-23
PRIOR FILING DATE: 2001-12-23
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-23
PRIOR PRIOR APPLICATION NUMBER: 60/259,308
PRIOR FILING DATE: 2001-12-23
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 11108
FEWARTH: FASTESC for Windows Version 4.0
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100.0%; Pred. No. 2.4e+02;
iive 0; Mismatches 0; Indels
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APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Undith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REPERENCE: ELITRA.0094 S. CORRENT APPLICATION NUMBER: US/09/741,669
CURRENT APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR PELING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SEQ ID NO 297
LENGTH: 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Haemophilus influenzae
US-09-815-242-11108
                                     Carr, Grant J.
Yamamoto, Robert T.
John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Escherichia coli
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Best Local Similarity
Matches 7; Conserva
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US-09-741-669-297
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ORGANISM:
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APPLICANT:
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; ORGANISM: Homo sapien
US-09-989-919-93
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US-09-864-761-40104
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Vamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REPERENCE: ELITRA.011A
CURRENT APPLICANTON NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                  0.8%; Score 7; DB 9; Length 104;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
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Pred. No. 2.4e+02
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-27

PRIOR PILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14107
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10348
LENGTH: 104
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-815-242-14107
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14107, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
US-10-287-274-323
'S Sequence 323, Application US/10287274
'Publication No. US20030181408A1
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                                                               ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10348
                                                                                                                                               Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conservat
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APPLICANT: Recipon, Herve

APPLICANT: Recipon, Herve

APPLICANT: Recipon, Herve

APPLICANT: Pluca, Jason

APPLICANT: Ghosh, Malavika

APPLICANT: Sun, Yongming

APPLICANT: Sun, Yongming

APPLICANT: Sun, Yongming

TILE REFERENCE: DEX-0289

CURRENT FILIG OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Prot

FILE REFERENCE: DEX-0289

CURRENT FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: 60/252,505

PRIOR FILING DATE: 2001-11-22

NUMBER OF SEQ ID NOS: 124

SOFTWARE: Patentin Version 3.1

LENGTH: 109

TYPE: PRI

ORCH.
                APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
FILE REFERNCE: ELITRA.OBDV1
CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
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Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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in. 2.4e+02;
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100.0%; Pred. No. 2.4
:ive 0; Mismatches
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                                                                                                                                PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11.09
PRIOR FILING DATE: 1999-11.09
PRIOR FILING DATE: 2000-11.09
NUMBER OF SEQ ID NOS: 469
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 323
LENGTH: 104
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R. Allyn
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; ORGANISM: Escherichia coli
US-10-287-274-323
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Best Local Similarity 10v..
Lac 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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LOCATION: (98) OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
1 LOCATION: (106)
2 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3972
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                    APPLICANT: Biree et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERCEE.

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

NUMBER: OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 3972

LENGTH: 115
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APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: SEKI, NACHIKO
APPLICANT: STEUNAMA TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: NACHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APPLICANT: NAGHARI, KENJI
APLICANT: NAGHARI, KENJI
FILE REFERENCE: 084335/016
CURRENT APPLICATION NUMBER: 105/050,435
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC_FEATURE LOCATION: (98)
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US-10-094-749-2223
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N: EXPRESSED IN HELA, SIGNAL = 3.9
N: EXPRESSED IN HELA, SIGNAL = 3
N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
N: EXPRESSED IN BEALN, SIGNAL = 5.4
N: EXPRESSED IN ADULT LIVER, SIGNAL = 4.4
N: EXPRESSED IN LUNG, SIGNAL = 5.5
N: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
N: EXT HUMAN HIT: AU129622.1, EVALUE 5.00e-42
N: SWISSPROT HIT: P35680, EVALUE 5.00e-43
IITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 114;
                                                                               CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-36
PRIOR FILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
                                  FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
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Best Local Similarity 100.0%; P.
Matches 7; Conservative 0;
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ORGANISM: Homo sapiens
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TYPE: PRT; CRGANISM: Homo sapiens US-10-094-749-2223

RESULT 38 US-10-26-4049-3972 'Sequence 3972, Application US/10264049 'Publication No. US20040005579A1

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Gaps

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0; Indels

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        Query Match
        0.8%; Score 7; DB 12; Length 116;

        Best Local Similarity 100.0%; Pred. No. 2.66+02;
        0, Gaps 0;

        Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
        0, Mismatches 0; Indels 0;

        Qy 357 AAAVGSA 21
        1 [|||||||

        Db 15 AAAVGSA 21
        1 SAAVGSA 21

        RESULT 40
        1 SAAVGSA 21

        RESULT 40
        1 SAAVGSA 21

        RESULT 40
        1 SAAVGSA 21

        RESULT 40
        1 SAAVGSA 21

        RESULT 40
        1 SAAVGSA 21

        Sequence 182, Application US/09739907
        1 SAAVGSA 21

        SENERAL INFORMATION: A Bull and Secreted Proteins
        1 TITLE OF INVENTION: 36 Human Secreted Proteins

        FILE REFERENCE: PROJOCI 220
        2 COURENT FILING DATE: 1999-07-07

        CURRENT FILING DATE: 1999-07-07
        3 PRIOR FILING DATE: 1999-01-07

        PRIOR FILING DATE: 1999-01-07
        3 PRIOR FILING DATE: 1999-01-07

        PRIOR PELICATION NUMBER: 60/070,567
        3 PRIOR PELICATION NUMBER: 60/070,658

        PRIOR APPLICATION NUMBER: 60/070,658
        3 PRIOR PELICATION NUMBER: 60/070,658

        PRIOR APPLICATION NUMBER: 60/070,658
        3 PRIOR FILING DATE: 1999-01-07

        PRIOR APPLICATION NUMBER: 60/070,658
        3 PRIOR FILING DATE: 1999-01-07

        PRIOR PRIORE: 1989-01-07<
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AAR22103 standard; Protein; 1098

AAR22103

06-JUL-1992

- LKT fusion protein. Bovine IL-2

Interleukin 2; leuko-toxin; vaccine; pneumonia; respiratory diseases

Pasteurella haemolytica

Bos taurus,

WO9203558-A

05-MAR-1992

91WO-CA00299 22-AUG-1991; 22-AUG-1990; 

90US-0571301

POTTER

Hughes HPA; Campos M, Potter A,

WPI; 1992-096901/12 N-PSDB; AAQ22771

- encodes fusion protein Interleukin 2-leuko-toxin gene fusion useful as vaccine for animal pneumonia

20; Fig 3; 68pp; English Claim

The IL-2-LKT protein was encoded by a chimeric gene contg. the bovine IL-2 gene fused to the DNA encoding at least one epitope of leukotoxin from P. haemolyvica. IL-2-LKT was gel purified and ligated into the expression vector pGH433 lac1. The resulting clone pAA356 (ATCC 68386) contd. the desired gene fusion under the control of the B. coli lac promoter. The protein produced by the gene fusion is useful in a vaccine compan. with a pharmaceutically acceptable vehicle, e.g. a carrier homologous to a rotavirus VP6 inner capsid protein. The vaccine can be used for preventing or ameliorating respiratory diseases in animals e.g. shipping fever pneumonia 

1098 AA; Sequence

See also AAR24124,5.

26; Length 1098; Indels Query Match 50.2%; Score 2332; DB 13; Best Local Similarity 50.1%; Pred. No. 9.9e-137; Matches 465; Conservative 174; Mismatches 264; Query Match Best Local S

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424 587 GTPIALLVAGVTGLISGILEASKQAMFESVANRLQGKILEWEKQNGGQNYFDKGYDSRYA 528 ASPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL 365 ò . 점

484 647 AYLANNLKFLSELNKELEAERVIAITQQRWDNNIGELAGITKLGERIKSGKAYADAFEDG 588 425 ò a

544 707 597 KKVBAGSNITLDAKTGIIDISNSNGKKTQALHFTSPLLTAGTESRERLTNGKYSYINKLK ---AETEGTDEIGLIVNAKAGNDDIFVGO FGRVKNWQVTDGEASSKLDFSKVIQRV---648 545 d

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                                            TLSSFLGTALAGIELDSLIKKGDAAPDALAKASIDLINEIIGNLSQSTOTIEAFSSQLAK 185
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                                                                                                                 LGSTISQAKGFSNIGNKLQNL-NFSKTNLGLEIITGLLSGISAGFALADKNASTGKKVAA 244
                                                                                                                             GPELSNOVIGNVTKAISSYVLAQRVAAGLSTTGAVAALITSSIMLAISPLAFMNAADKFN 304
                                                                                                                                                                      HANALDEFAKOFRKFGYDGDHLLAEYQRGVGTIEASLTTISTALGAVSAGVSAAAVGSAV 364
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                                                                                                                                                                                                                                                      SPIALLVSGITGVISTILQYSKQAMFEHVANKIHNKIVEWEKNNHGKNYFENGYDARYL 587
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Bovine IL-2/Pasteurella haemolytica leukotoxin fusion protein.

(first entry)

19-DEC-2000

AAB21073;

AAB2107: ID AAI XX AAI AC AAI XX AAI XX DT 19

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AAB21073 standard; Protein; 1098

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immunogenic chimeric protein that comprises gamma-interferon (gamma-IFN) or an active fragment thereof, linked to an epitope of a Pasteurella haemolytica leukotoxin (kTr). Pasteurella species, especially pasteurella haemolytica, are responsible for respiratory diseases in a range of agricultural animals, most particularly cattle, but also sheep, pigs, horses and fowl. Shipping fever is the most economically important respiratory disease associated with Pasteurella species, affecting 15-30% of exposed cattle and resulting in a 2-5% mortality rate in the exposed population. The vaccine composition of the invention is is useful for preventing or ameliorating respiratory diseases such as pneumonia, particularly shipping fever pneumonia, in livestock. The present sequence represents a fusion protein comprising bovine interleukin-2 (IL-2) and pasteurella haemolytica leukotoxin, which may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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Bovine IL-2; interleukin-2; leukotoxin; LKT; respiratory disease;
pneumonia; shipping fever; cattle; livestock; anti-Pasteurella vaccine;
immunogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine for stimulating immunity against pneumonia comprises chimeric protein comprising gamma-interferon and leukotoxin derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also be used as an anti-Pasteurella vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column 31-38; 56pp; English.
                                                                                               haemolytica
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CIBA GEIGY CANADA LTD
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96US-0681479
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91US-0777715
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FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH,
     JICST-EPLUS, JAPIO' ENTERED AT 09:57:43 ON 18 FEB 2004
                                                                            - Author(s)
              24 S "FARN J"?/AU
L1
              390 S "STRUGNELL R"?/AU
L2
              186 S "TENNENT J"?/AU
L3
                7 S L1 AND L2 AND L3
L4
L5
                8 S L1 AND (L2 OR L3)
                7 S L2 AND L3
L6
               49 S (L1 OR L2 OR L3) AND BOVIS
L7
    A. .
               50 S L4 OR L5 OR L6 OR L7
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              13 DUP REM L8 (37 DUPLICATES REMOVED)
L9
     ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
                            2001:168028 HCAPLUS
ACCESSION NUMBER:
                             134:221433
DOCUMENT NUMBER:
                            Vaccine antigens of Moraxella
TITLE:
                             Farn, Jacinta; Strugnell,
INVENTOR(S):
                            Richard; Tennent, Jan
                             Commonwealth Scientific and Industrial Research
PATENT ASSIGNEE(S):
                             Organisation, Australia; The University of
                            Melbourne
                             PCT Int. Appl., 60 pp.
SOURCE:
                             CODEN: PIXXD2
DOCUMENT TYPE:
                             Patent
LANGUAGE:
                            English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:
     PATENT NO.
                         KIND DATE
                                                 APPLICATION NO.
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                               _____
      ______
                                           WO 2000-AU1048 20000831
     WO 2001016172 A1 20010308
          W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
               TJ, TM
          RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
              CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                                               EP 2000-955974 20000831
                         A1 20020605
     EP 1210364
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC,
               PT, IE, SI, LT, LV, FI, RO, MK, CY, AL
                        A 20020611
                                                 BR 2000-13574
     BR 2000013574
                                                                     20000831
                                              AU 1999-2571 A 19990831
PRIORITY APPLN. INFO.:
                                                                W 20000831
                                              WO 2000-AU1048
     The present invention relates to antigens of Moraxella, in
AB
     particular, Moraxella bovis, nucleic acid sequences
     encoding these antigens and formulations for use in raising an
      immune response against Moraxella.
                                    THERE ARE 5 CITED REFERENCES AVAILABLE FOR
REFERENCE COUNT:
                             5
                                    THIS RECORD. ALL CITATIONS AVAILABLE IN
                                    THE RE FORMAT
     ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
1.9
                             2001:811555 HCAPLUS
ACCESSION NUMBER:
```

Searcher : Shears 571-272-2528

136:66038

DOCUMENT NUMBER:

Molecular characterization of a secreted enzyme TITLE:

with phospholipase B activity from Moraxella

Farn, Jacinta L.; Strugnell; AUTHOR(S):

Richard A.; Hoyne, Peter A.; Michalski,

Wojtek P.; Tennent, Jan M.

CSIRO Livestock Industries, Geelong, 3220, CORPORATE SOURCE:

Australia

Journal of Bacteriology (2001), 183(22), SOURCE:

6717-6720

CODEN: JOBAAY; ISSN: 0021-9193 American Society for Microbiology

PUBLISHER: DOCUMENT TYPE: Journal English LANGUAGE:

A candidate for a vaccine against infectious bovine AB

keratoconjunctivitis (IBK) has been cloned and characterized from Moraxella bovis. The plb gene encodes a protein of 616 amino acids (mol. mass of .apprx.65.8 kDa) that expresses

phospholipase B activity. Amino acid sequence anal. revealed that

PLB is a new member of the GDSL (Gly-Asp-Ser-Leu) family of

lipolytic enzymes.

THERE ARE 32 CITED REFERENCES AVAILABLE . 32 REFERENCE COUNT:

FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3 L9

ACCESSION NUMBER: DOCUMENT NUMBER:

2000:359019 HCAPLUS 133:100763

TITLE:

Characterization of hemolysin of Moraxella

bovis using a hemolysis-neutralizing

monoclonal antibody

Billson, F. Mark; Harbour, Colin; Michalski, AUTHOR(S):

Wojtek P.; Tennent, Jan M.; Egerton,

John R.; Hodgson, Jennifer L.

Department of Veterinary Clinical Sciences, CORPORATE SOURCE:

University of Sydney, Camden, 2570, Australia

Infection and Immunity (2000), 68(6), 3469-3474 -SOURCE:

CODEN: INFIBR; ISSN: 0019-9567 American Society for Microbiology

PUBLISHER: DOCUMENT TYPE: Journal

English LANGUAGE:

A concentrated bacterial culture supernatant from the hemolytic Moraxella AB bovis strain UQV 148NF was used to immunize mice and

generate monoclonal antibodies (MAbs). One, MAb G3/D7, neutralized

the hemolytic activity of M. bovis and recognized a 94-kDa

protein by Western blot anal. in hemolytic M. bovis strains representing each of the different fimbrial serogroups.

Exposure of corneal epithelial cells to M. bovis concentrated culture supernatants demonstrated a role for an exotoxin in the pathogenesis of infectious bovine keratoconjunctivitis, while neutralization of hemolytic and cytotoxic activities by MAb G3/D7 implies that these activities are related or have common epitopes.

The action of M. bovis hemolysin was further characterized

in sheep erythrocyte prepns. with a binding step and Ca2+ required

for lysis to proceed, similar to the RTX family of bacterial exotoxins. Neutralization of lytic activity in vitro is evidence

for the presence of M. bovis antigens, which may be

capable of protecting cattle from the development of infectious

Searcher : Shears 571-272-2528

bovine keratoconjunctivitis.

THERE ARE 39 CITED REFERENCES AVAILABLE REFERENCE COUNT:

FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 4 L9

2000:507582 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 133:249416

Identification of type 4 fimbriae in TITLE:

Actinobacillus pleuropneumoniae

Zhang, Y.; Tennent, J. M.; Ingham, A.; AUTHOR(S):

Beddome, G.; Prideaux, C.; Michalski, W. P. Private Bag 24, Australian Animal Health CORPORATE SOURCE:

Laboratory, CSIRO Animal Health, Geelong, 3220,

Australia

FEMS Microbiology Letters (2000), 189(1), 15-18 SOURCE:

CODEN: FMLED7; ISSN: 0378-1097

Elsevier Science B.V. PUBLISHER:

DOCUMENT TYPE: Journal English LANGUAGE:

Type 4 fimbriae have been identified on the cell surface of AB Actinobacillus pleuropneumoniae by electron microscopy and

N-terminal sequencing anal. A. pleuropneumoniae type 4 fimbrial subunit protein, purified from cell cultures and from outer membrane

prepns., reacted with polyclonal antibody raised against type 4 fimbriae of Moraxella bovis on Western blots. N-terminal sequence anal. of the purified 17 kDa type 4 fimbrial subunit protein, named ApfA, revealed the first 12 amino acids to be identical to those of other type 4 fimbrial subunit proteins.

THERE ARE 23 CITED REFERENCES AVAILABLE REFERENCE COUNT: 23

FOR THIS RECORD. ALL CITATIONS AVAILABLE

IN THE RE FORMAT

ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5 L9

1997:19161 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 126:57234

Identification, purification, and TITLE:

characterization of the type 4 fimbriae of

Pasteurella multocida

Ruffolo, Carmel G.; Tennent, Jan M.; AUTHOR(S):

Michalski, Wojtek P.; Adler, Ben

Dep. Microbiology, Monash Univ., Clayton, 3168, CORPORATE SOURCE:

Australia

Infection and Immunity (1997), 65(1), 339-343 SOURCE:

CODEN: INFIBR; ISSN: 0019-9567

American Society for Microbiology PUBLISHER:

DOCUMENT TYPE: Journal English LANGUAGE:

The presence of fimbriae on Pasteurella multocida has been reported,

but there have been no prior studies aimed at conclusively characterizing these structures. We now report on the

identification and characterization of type 4 fimbriae on serogroup

A, B, and D strains of P. multocida. Under microaerophilic conditions P. multocida showed an increased expression of the

fimbriae, which were observed to form bundles. Fimbriae purified by high-performance reverse-phase liquid chromatog. constituted a single 18-kDa subunit, the first 21 amino acids of which shared very high similarity with the N-terminal amino acids sequence of other type 4

> Shears 571-272-2528 Searcher :

fimbrial subunits. Antiserum against the P. multocida 18-kDa protein immunostained the type 4 fimbrial subunit of Moraxella **bovis** and Dichelobacter nodosus. Based on these observations we conclude that P. multocida possesses type 4 fimbriae and have designated the P. multocida fimbrial subunit Ptf/A.

L9 ANSWER 6 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on

STN

ACCESSION NUMBER: 1996:399092 BIOSIS DOCUMENT NUMBER: PREV199699121448

TITLE: Construction of a defined aromatic mutant of the

gram-positive bacterium C. pseudotuberculosis.

AUTHOR(S): Simmons, Cameron [Reprint author]; Farn,

Jacinta [Reprint author]; Strugnell,
Richard [Reprint author]; Hodgson, Adrian

CORPORATE SOURCE: Dep. Microbiol., Univ. Melbourne, Parkville, VIC

3052, Australia

SOURCE: Brown, F. [Editor]; Norrby, E. [Editor]; Burton, D.

[Editor]; Mekalanos, J. [Editor]. Vaccines (Cold Spring Harbor), (1996) pp. 111-116. Vaccines (Cold Spring Harbor); Molecular approaches to the control

of infectious diseases.

Publisher: Cold Spring Harbor Laboratory Press, 10

Skyline Drive, Plainview, New York 11803, USA.

Series: Vaccines (Cold Spring Harbor).

Meeting Info.: Thirteenth Meeting. Cold Spring Harbor, New York, USA. September 13-17, 1995.

ISSN: 0899-4056. ISBN: 0-87969-479-3.

DOCUMENT TYPE: Book

Conference; (Meeting)
Book; (Book Chapter)

Conference; (Meeting Paper)

LANGUAGE: English

ENTRY DATE: Entered STN: 3 Sep 1996

Last Updated on STN: 3 Sep 1996

L9 ANSWER 7 OF 13 MEDLINE on STN DUPLICATE 6

ACCESSION NUMBER: 95336598 MEDLINE DOCUMENT NUMBER: PubMed ID: 7542003

TITLE: Antibody reactivity to mycobacterial 65 kDa heat

shock protein: relevance to autoimmunity.

AUTHOR: Karopoulos C; Rowley M J; Handley C J; Strugnell

R A

CORPORATE SOURCE: Department of Biochemistry, Monash University,

Clayton, Victoria, Australia.

SOURCE: Journal of autoimmunity, (1995 Apr) 8 (2) 235-48.

Journal code: 8812164. ISSN: 0896-8411.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199508

ENTRY DATE: Entered STN: 19950905

Last Updated on STN: 19960129 Entered Medline: 19950818

AB Reactivity to the mycobacterial 65 kDa heat shock protein (HSP 65) has been implicated in the pathogenesis of adjuvant arthritis in the rat, and may be involved in the pathogenesis of rheumatoid arthritis

Searcher: Shears 571-272-2528

or other autoimmune diseases in humans. Accordingly this study sought quantitative or qualitative differences in the antibody reactivity to HSP 65 between normal controls, patients with the multisystem autoimmune diseases, rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE) and patients with the mycobacterial infections, tuberculosis (TB) and leprosy. Levels of antibodies to recombinant HSP 65 in serum were measured by ELISA in normal subjects and in patients with RA, SLE, TB or leprosy. Antibody reactivity was examined by Western blotting using polypeptide fragments of HSP 65 derived by recombinant DNA techniques, or by digestion with trypsin or cyanogen bromide (CNBr). Reactivity to a synthetic peptide, the adjuvant arthritis T-cell epitope of HSP 65 (180-188), was tested by ELISA. High levels of antibodies to full length recombinant HSP 65 from Mycobacterium bovis were present in all the groups tested. By Western blot analysis, most reactivity with intact HSP 65 was retained in a 32 kDa tryptic fragment, judged by sequencing and size estimations to represent amino acid residues 118- approximately 388. sequence included a major T-cell epitope for adjuvant arthritis (180-188), but these nine amino acids were not essential for B-cell reactivity since most sera also reacted with residues 188-540 which lack the T-cell epitope. Moreover, the 180-188 synthetic peptide was unreactive by ELISA, and did not inhibit reactivity with the intact recombinant HSP 65. In conclusion, most individuals had antibodies to mycobacterial HSP 65, presumably resulting from previous bacterial infections. The magnitude of the response was unrelated to the occurrence of systemic autoimmune disease, and the pattern of antibody reactivity with recombinant and proteolytic fragments of HSP 65 suggests that the major B-cell epitope is conformational and consists of discontinuous regions of the molecule.

ANSWER 8 OF 13 MEDLINE on STN DUPLICATE 7 MEDLINE

ACCESSION NUMBER: 96037961

PubMed ID: 7571364 96037961

DOCUMENT NUMBER:

The protective efficacy of cloned Moraxella TITLE:

bovis pili in monovalent and multivalent

vaccine formulations against experimentally induced

infectious bovine keratoconjunctivitis (IBK).

Lepper A W; Atwell J L; Lehrbach P R; Schwartzkoff C AUTHOR:

L; Egerton J R; Tennent J M

CSIRO Division of Animal Health, Animal Health CORPORATE SOURCE:

Research Laboratory, Parkville, Vic., Australia.

VETERINARY MICROBIOLOGY, (1995 Jul) 45 (2-3) 129-38. SOURCE:

Journal code: 7705469. ISSN: 0378-1135.

PUB. COUNTRY: Netherlands (CLINICAL TRIAL)

DOCUMENT TYPE: (CONTROLLED CLINICAL TRIAL)

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199511

Entered STN: 19951227 ENTRY DATE:

Last Updated on STN: 19951227 Entered Medline: 19951108

Calves were vaccinated with cloned Moraxella bovis pili of AB serogroup C (experiment 1) or B (experiment 2) either as a monovalent formulation or as part of a multivalent preparation with

> Searcher : Shears 571-272-2528

pili of six other serogroups. Within 4 weeks of the second vaccine dose vaccinated calves and non-vaccinated controls were challenged via the ocular route with either virulent M. bovis strain Dal2d (serogroup C) or M. bovis strain 3WO7 (serogroup B) in experiments 1 and 2, respectively. Calves vaccinated with multivalent vaccines had significantly lower antibody titres than those vaccinated with monovalent preparations. Nevertheless, the levels of protection against infectious bovine keratoconjunctivitis (IBK) achieved with multivalent vaccines were 72% and 83% for the groups challenged with M. bovis strains of serogroups B and C, respectively. The serogroup C monovalent vaccine gave 100% protection against experimentally induced IBK and M. bovis isolates cultured from the eyes 6 days post-challenge were identified as belonging solely to serogroup C. Unexpectedly, only 25% protection was achieved against homologous strain challenge of calves that received the monovalent serogroup B vaccine. Furthermore, the majority of M. bovis isolates recovered from calves in this group belonged to serogroup C, as did half of those isolates cultured from the multivalent vaccinates. remaining bacterial isolates from the latter group, together with all isolates from the non-vaccinated controls, belonged to serogroup Results are consistent with the hypothesis that derivatives of the serogroup B challenge inoculum had expressed serogroup C pilus antigen within 6 days of the challenge, possibly as a result of pilus gene inversion occurring in response to the presence of specific antibody in eye tissues and tears.

ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 8 L9

ACCESSION NUMBER: DOCUMENT NUMBER:

1994:694086 HCAPLUS 121:294086

TITLE:

Characterization of pilin genes from seven serologically defined prototype strains of

Moraxella bovis

AUTHOR(S):

Atwell, John L.; Tennent, Jan M.; Lepper, Anthony W. D.; Elleman, Tom C.

CORPORATE SOURCE:

Commonwealth Scientific and Industrial Research

Organisation, Victoria, 3052, Australia

SOURCE:

Journal of Bacteriology (1994), 176(16), 4875-82

CODEN: JOBAAY; ISSN: 0021-9193

DOCUMENT TYPE:

Journal English

LANGUAGE:

Numerous field isolates of Moraxella bovis have previously AΒ been classified by serol. techniques into seven serogroups, each defined by homologous cross-reaction with antisera prepared against purified pili of a single prototype strain. The gene encoding pilin from each of the prototype strains has been characterized by nucleotide sequence determination The coding sequences show extensive homol. (70 to 80%) while the strains were also characterized. The presence of an addnl., partial pilin gene in each prototype strain was confirmed by Southern blot anal., and the partial pilin genes from two strains of one serogroup were characterized by sequence determination Features of the pilin gene sequences are considered in relation to pilin gene inversion and the serol. variants which may arise from inversion events.

ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 9

ACCESSION NUMBER:

1995:236681 HCAPLUS

TITLE:

A haemolytic cell-free preparation of Moraxella

Searcher : Shears 571-272-2528

bovis confers protection against

Infectious Bovine Keratoconjunctivitis

AUTHOR(S):

Billson, F. Mark; Hodgson, Jennifer L.; Egerton, John R.; Lepper, Anthony W. D.; Michalski, Wojtek P.; Schwartzkoff, C. Leigh; Lehrbach,

Philip R.; Tennent, Jan M.

University of Sydney, Department of Animal CORPORATE SOURCE:

Health, Private Bag 3, Camden, NSW, 2570,

Australia

FEMS Microbiology Letters (1994), 124(1), 69-74 SOURCE:

CODEN: FMLED7; ISSN: 0378-1097

Elsevier PUBLISHER: DOCUMENT TYPE: Journal English LANGUAGE:

Protection conferred by a cell-free preparation from a haemolytic AB Moraxella bovis isolate, UQV 148NF, was compared to an equivalent fraction from a non-haemolytic M. bovis isolate, Gordon 26L3, and to a recombinant DNA-derived pili vaccine. Three groups of ten calves were vaccinated twice with one of the three prepns. and, together with ten non-vaccinated calves, challenged with virulent M. bovis isolate Dal 2d. Compared to the control group, significant protection was observed in the group receiving the pili vaccine and the group receiving the preparation from haemolytic isolate, UQV 148NF.

DUPLICATE 10 MEDLINE on STN ANSWER 11 OF 13 L9

ACCESSION NUMBER:

94055030 MEDLINE

DOCUMENT NUMBER:

PubMed ID: 7901935 94055030

TITLE:

A Moraxella bovis pili vaccine produced by

recombinant DNA technology for the prevention of

infectious bovine keratoconjunctivitis.

AUTHOR:

Lepper A W; Elleman T C; Hoyne P A; Lehrbach P R;

Atwell J L; Schwartzkoff C L; Egerton J R;

Tennent J M

CORPORATE SOURCE:

CSIRO Division of Animal Health, Animal Health Research Laboratory, Parkville, Vic., Australia. VETERINARY MICROBIOLOGY, (1993 Jul) 36 (1-2) 175-83.

SOURCE:

Journal code: 7705469. ISSN: 0378-1135.

PUB. COUNTRY:

Netherlands

DOCUMENT TYPE: LANGUAGE:

Journal; Article; (JOURNAL ARTICLE)

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199312

ENTRY DATE:

Entered STN: 19940117

Last Updated on STN: 19970203 Entered Medline: 19931203

Pili (fimbriae) were prepared from Moraxella bovis strain AB Dalton 2d (Dal2d) and from a derivative of Pseudomonas aeruginosa K/2PfS that contained a plasmid-borne Dal2d pilin gene and produced pili having serogroup-specific identity to Dal2d. Nine calves were vaccinated with two doses each of 30 micrograms authentic M. bovis Dal2d pili in oil adjuvant and 10 calves were vaccinated with a similar dose of P. aeruginosa-derived Dal2d pili in the same formulation. All 19 calves and 10 non-vaccinated controls were challenged by instillation of 1  $\times$  10(9) virulent M. bovis Dal2d cells into both conjunctival sacs 19 days after the second vaccine dose. The serological response to vaccination and the degree of protection against experimentally induced

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infectious bovine keratoconjunctivitis (IBK) were assessed. None of the nine calves vaccinated with authentic M. bovis Dal2d pili developed IBK while two of those vaccinated with P. aeruginosa-derived Dal2d pili developed lesions which accounted for a mean group lesion score of 0.3. In contrast, 9 of the 10 non-vaccinated calves developed IBK lesions, the majority of which were progressive, required early treatment and accounted for a mean group lesion score of 1.5. These results demonstrate the potential of a relatively low dose of pili produced by recombinant DNA technology for development of an effective vaccine against IBK.

1.9 ANSWER 12 OF 13 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on

1993:200425 BIOSIS ACCESSION NUMBER: PREV199344096675 DOCUMENT NUMBER:

Purification of proteases by immobilised bacitracin A TITLE:

affinity chromatography.

Michalski, Wojtek P.; Crooks, Jennipher K.; Prowse, AUTHOR(S):

Stephen J.; Tennent, Jan M.; Lepper,

Anthony W. D.

CSIRO Div. Anim. Health, Anim. Health Res. Lab., CORPORATE SOURCE:

Private Bag No. 1, Parkville, Victoria 3052,

Australia

Journal of Cellular Biochemistry Supplement, (1993) SOURCE:

Vol. 0, No. 17 PART A, pp. 50.

Meeting Info.: Keystone Symposium on Protein

Purification and Biochemical Engineering. Santa Fe,

New Mexico, USA. January 15-21, 1993.

ISSN: 0733-1959.

Conference; (Meeting) DOCUMENT TYPE:

LANGUAGE:

English

ENTRY DATE: Entered STN: 16 Apr 1993

Last Updated on STN: 9 Jun 1993

DUPLICATE 11 MEDLINE on STN T.9 ANSWER 13 OF 13

93069932 ACCESSION NUMBER:

MEDLINE

PubMed ID: 1359693 93069932 DOCUMENT NUMBER:

The protective efficacy of pili from different TITLE:

strains of Moraxella bovis within the same

serogroup against infectious bovine

keratoconjunctivitis.

Lepper A W; Moore L J; Atwell J L; Tennent J AUTHOR:

CORPORATE SOURCE: CSIRO Division of Animal Health, Animal Health

Research Laboratory, Parkville, Vic., Australia. VETERINARY MICROBIOLOGY, (1992 Sep) 32 (2) 177-87.

SOURCE:

Journal code: 7705469. ISSN: 0378-1135.

Netherlands PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE) DOCUMENT TYPE:

LANGUAGE: English

Priority Journals FILE SEGMENT:

199212 ENTRY MONTH:

Entered STN: 19930122 ENTRY DATE:

Last Updated on STN: 19970203 Entered Medline: 19921218

Three groups of ten calves were each immunised with a total of 400 AB micrograms pili prepared from three separate strains of Moraxella bovis in Alhydrogel-oil adjuvant as two divided, equal doses

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21 days apart. Groups 1 and 2 each received a monovalent vaccine made from strain 4L and S276R respectively, which belonged to pili serogroup A. Group 3 received vaccine made from pili of strain Maffl, belonging to serogroup F. A further group of ten calves served as non-vaccinated controls. Calves in groups 1 and 2 had developed serogroup A-specific antibody and those in group 3 developed serogroup F-specific antibody, and some evidence of cross-reacting antibody was also detected when measured by an agglutination test using formalin-killed piliated cells of serogroup A strain 4L. Although antibody titres measured against purified pili by ELISA were highest with homologous serogroup antigens, cross-reactive titres to shared epitopes of M. bovis pili were also detected by this method. Ocular challenge of the 40 calves with virulent M. bovis of serogroup A strain S276R was carried out 14 days after the second vaccine dose. All non-vaccinated calves developed infectious bovine keratoconjunctivitis (IBK). The percentage protection in groups 1 (strain 4L) and 2 (strain S276R) was 60% and 80% respectively (P less than 0.05), with mean lesion scores of 0.7 and 0.3 out of a possible 6.0. The percentage protection of calves in group 3 (strain Maff1) was only 30%, with a mean lesion score of 1.4 compared with 2.2 for non-vaccinated controls. The present findings, together with other evidence indicating that immunity to IBK is serogroup-specific, suggest that inclusion of pili from one representative strain from each of the seven Australian and British serogroups in a polyvalent, subunit vaccine should effectively protect the majority of cattle against IBK caused by most field strains of M. bovis encountered in Australia and the United Kingdom.

(FILE 'HCAPLUS, MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 10:01:50 ON 18 FEB 2004)

L10 45 S (L1 OR L2 OR L3) AND MORAXELLA L11 0 S L10 NOT L8

FILE 'HOME' ENTERED AT 10:02:32 ON 18 FEB 2004